

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:20 ; Search time 127.123 Seconds
(without alignments) 256
568.992 Million cell updates/sec

Title: US-10-067-122B-2
Perfect score: 1428
Sequence: 1 MGNVCNVVVIVLLVGCCK.....DACSRCPOEERGGGGYEL 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep_29Jan04:.*
1: Genesep1980s:.*
2: Genesep1990s:.*
3: Genesep2000s:.*
4: Genesep2001s:.*
5: Genesep2002s:.*
6: Genesep2003as:.*
7: Genesep2003bs:.*
8: Genesep2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1428	100.0	256	2 AAR64199	Aar64199 Murine 4-
2	1428	100.0	256	2 AAR70978	Aar70978 4-1BB rec
3	1428	100.0	256	2 AAW04173	Aaw04173 Mouse rec
4	1428	100.0	256	2 AAW26659	Aaw26659 Mouse 4-1
5	1428	100.0	256	2 AAY28687	Aay28687 Mouse Rec
6	1428	100.0	256	2 AAY33215	Aay33215 Murine CD
7	1428	100.0	256	5 AAE22581	Aae22581 Mouse rec
8	1428	100.0	256	5 ABB75954	Abb75954 Murine cy
9	1428	100.0	256	7 ADC25939	Adc25939 Murine re
10	1428	100.0	256	7 ADE87549	Ade87549 Mouse rec
11	1085	76.0	191	4 AAB66986	Aab66986 4lbb prot
12	795	55.7	255	2 AAR64197	Aar64197 Human 4-1
13	795	55.7	255	2 AAR70977	Aar70977 H4-1BB re
14	795	55.7	255	2 AAW26658	Aaw26658 Human 4-1
15	795	55.7	255	2 AAY28688	Aay28688 Human rec
16	795	55.7	255	2 AAY33214	Aay33214 Human CD1
17	795	55.7	255	4 AAE08546	Aae08546 Human h4-
18	795	55.7	255	4 AAB50521	Aab50521 Human tum
19	795	55.7	255	5 ABR375955	Abr375955 Human cyt
20	795	55.7	255	6 ABR39863	Abr39863 Human MOC
21	795	55.7	255	6 ABB84640	Abb84640 Human h4-
22	795	55.7	255	7 AAE39531	Aae39531 Human pro
23	795	55.7	255	7 ADE37803	Ade37803 Human PRO
24	795	55.7	255	7 ADD25599	Add25599 Binding d
25	795	55.7	255	7 ADE87541	Ade87541 Unknown h

26	782	54.8	255	2 AAW04174	Aaw04174 Human rec
27	768	53.8	255	2 AAR74087	Aar74087 Human rec
28	656	45.9	219	2 AAW31759	Aaw31759 A novel h
29	656	45.9	219	2 AAW92523	Aaw92523 Human h4-
30	656	45.9	219	2 AAW92524	Aaw92524 Human h4-
31	656	45.9	219	4 AAE08545	Aae08545 Human h4-
32	656	45.9	219	6 ABB84639	Abb84639 Human h4-
33	499	34.9	132	3 AAY94714	Aay94714 Tumour ne
34	268	18.8	69	2 AAW94650	Aaw94650 TNF-R ext
35	268	18.8	69	4 AAB69202	Aab69202 Human TNF
36	237	16.6	415	4 AAB36700	Aab36700 Human tum
37	237	16.6	415	6 ABB96138	Abb96138 Mouse lym
38	215	15.1	625	2 AAW83200	Aaw83200 Murine OS
39	215	15.1	625	2 AAW69958	Aaw69958 Murine NF
40	215	15.1	625	2 AAW68294	Aaw68294 Murine NF
41	215	15.1	625	2 AAE08739	Aae08739 Murine re
42	215	15.1	625	3 AAY53649	Aay53649 A mouse r
43	215	15.1	625	3 AAY59509	Aay59509 OBM bindi
44	215	15.1	625	4 AAE04427	Aae04427 Murine re
45	215	15.1	625	4 AAE01994	Aae01994 Murine RA

ALIGNMENTS

RESULT 1
ID AAR64199 standard; protein; 256 AA.
XX AAR64199;

AC AAR64199;
XX 25-MAR-2003 (revised)
DT 08-AUG-1995 (first entry)
XX Murine 4-1BB polypeptide.
DE Murine 4-1BB polypeptide.

XX T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
XX Mus musculus.

OS Mus musculus.

XX WO9426290-A1.

XX 24-NOV-1994.

XX 06-MAY-1994; 94WO-US005036.

XX 07-MAY-1993; 93US-00060843.

XX (IMMV) IMMUNEX CORP.

XX Goodwin RG, Smith CA, Alderson MR;

XX WPI; 1995-022265/03.

XX N-PSDB; AAQ75428.

XX Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB to transduce signal.

XX Example 1; Page 44-45; 65pp; English.

XX The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75422) are useful in a pharmaceutical composition for stimulating the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring mechanisms of T-cell activation, as they are expressed on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation of primary T-cells during the derivation of clonal T-cell lines. It may also be used to stimulate proliferation of activated T-cells, used in therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 256 AA;

Query Match 100.0%; Score 1428; DB 2; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.7e-109;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCYVIVVILLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPSTFSSIGGQPN 60
DB 1 MGNVCYVIVVILLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPSTFSSIGGQPN 60

QY 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPGQCTRCCKDCRPGQELTKQCKTCS 120
DB 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPGQCTRCCKDCRPGQELTKQCKTCS 120

QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVCGPPVVSFSPSTTISVTPEGGPG 180

QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKPKFPHIFKQPKKTTGAAQEDACS 240
DB 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKPKFPHIFKQPKKTTGAAQEDACS 240

QY 241 CRCPQEEGGGGYEL 256
DB 241 CRCPQEEGGGGYEL 256

RESULT 2
AAR70978
ID AAR70978 standard; protein; 256 AA.
XX AC AAR70978;
XX DT 25-MAR-2003 (revised)
XX DT 16-OCT-1995 (first entry)
XX DE 4-1BB receptor protein.
XX KW 4-1BB; receptor protein; immunosuppressive; autoimmune disease;
XX KW organ transplantation; cell membrane ligand.
XX OS Mus sp.
XX PH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT /label= Sig_peptide
XX PN WO9507984-A1.
XX PD 23-MAR-1995.
XX PF 15-SEP-1994; 94WO-US010457.
XX PR 16-SEP-1993; 93US-00122796.
XX PA (INDV) UNIV INDIANA FOUND.
XX PI Kwon BS;
XX WPI; 1995-131352/17.
XX N-PSDB; AAQ86127.
XX Novel cDNA encoding human receptor protein H4-1BB - useful to produce the
XX protein which is used to treat autoimmune disease and facilitate organ
XX transplantation.
XX Disclosure; Fig 1; 36pp; English.
XX CC cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was
XX isolated using PCR primers based on the homologous mouse 4-1BB gene
XX (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR
XX -2003 to correct PN field.)
XX SQ Sequence 256 AA;
XX Query Match 100.0%; Score 1428; DB 2; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.7e-109;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCYVIVVILLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPSTFSSIGGQPN 60
DB 1 MGNVCYVIVVILLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPSTFSSIGGQPN 60

QY 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPGQCTRCCKDCRPGQELTKQCKTCS 120
DB 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPGQCTRCCKDCRPGQELTKQCKTCS 120

QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVCGPPVVSFSPSTTISVTPEGGPG 180

QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKPKFPHIFKQPKKTTGAAQEDACS 240
DB 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKPKFPHIFKQPKKTTGAAQEDACS 240

QY 241 CRCPQEEGGGGYEL 256
DB 241 CRCPQEEGGGGYEL 256

RESULT 3
AAW04173
ID AAW04173 standard; protein; 256 AA.
XX AC AAW04173;
XX DT 12-DEC-1996 (first entry)
XX DE Mouse receptor 4-1BB.
XX KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
XX KW immunostimulant; cancer; autoimmune disease; graft rejection; therapy.
XX OS Mus sp.
XX PN WO9629348-A1.
XX PD 26-SEP-1996.
XX PF 22-MAR-1996; 96WO-US003965.
XX PR 23-MAR-1995; 95US-00409851.
XX PA (INDV) UNIV INDIANA FOUND.
XX PI Kwon BS, Kang C;
XX WPI; 1996-443138/44.
XX N-PSDB; AAT39541.
XX Monoclonal antibody specific for human receptor protein 4-1BB - used to
XX enhance proliferation and activation of T-cells for treatment of cancer
XX and to inhibit specific ligand binding for treating autoimmune diseases.
XX Disclosure; Page 32-34; 48pp; English.
XX CC Novel murine receptor protein 4-1BB (AAW04173) has the potential to
XX function as an accessory signaling molecule during T-cell activation and
XX proliferation. It may represent a cell surface molecule involved in T-
XX cell-APC interactions and may also act as a B-cell costimulator. It is
XX structurally related to members of the nerve growth factor receptor
XX superfamily. Its amino acid sequence was deduced from an isolated cDNA
XX clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was
XX identified and used to raise a monoclonal antibody useful in cancer and
XX autoimmune disease therapy
XX SQ Sequence 256 AA;
XX Query Match 100.0%; Score 1428; DB 2; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.7e-109; Mismatches 0; Indels 0; Gaps 0; Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
DB 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVACGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQCKTCS 120
DB 61 CNICRVACGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHFKQPKKTTGAQBEDACS 240
DB 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHFKQPKKTTGAQBEDACS 240
QY 241 CRCPQEEGGGGYEL 256
DB 241 CRCPQEEGGGGYEL 256

RESULT 4
AAW26659 standard; protein; 256 AA.
ID AAW26659
XX AC AAW26659;
XX AC AAW26659;
DT 25-MAR-2003 (revised)
DT 25-FEB-1998 (first entry)
XX AC AAW26659;
DE Mouse 4-1BB receptor.
XX 4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell;
KW proliferation; immunostimulant.
XX Mus musculus.
XX Key Location/Qualifiers
FH Peptide 1. .23
FT /label= sig_peptide
XX US5674704-A.
XX 07-OCT-1997.
XX 06-MAY-1994; 94US-00236918.
XX 07-MAY-1993; 93US-00060843.
XX (IMV) IMMUNEX CORP.
XX Alderson MR, Goodwin RG, Smith CA;
XX WPI; 1997-502333/46.
XX N-PSDB; AAT91027.
XX DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell
XX proliferation in vitro, and as research tools.
XX Disclosure; Col 39-40; 32pp; English.
XX This protein comprises mouse 4-1BB, a member of the tumour necrosis
XX factor receptor superfamily that is expressed on helper, suppressor and
XX cytolytic T cells, as well as on mouse brain tissue. A novel claimed
XX cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned
XX and sequenced (see AAW26656) that binds to murine 4-1BB. 4-1BB-L,
XX especially its soluble extracellular domain, can be used to stimulate T-
XX cell proliferation in vitro, as a research tool and as an affinity ligand
XX for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 256 AA;
Query Match 100.0%; Score 1428; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.7e-109; Mismatches 0; Indels 0; Gaps 0; Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
DB 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVACGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQCKTCS 120
DB 61 CNICRVACGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHFKQPKKTTGAQBEDACS 240
DB 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHFKQPKKTTGAQBEDACS 240
QY 241 CRCPQEEGGGGYEL 256
DB 241 CRCPQEEGGGGYEL 256

RESULT 5
AAW28687 standard; protein; 256 AA.
ID AAW28687
XX AC AAW28687;
DT 13-OCT-1999 (first entry)
XX Mouse Receptor 4-1BB protein.
XX Mouse Receptor 4-1BB cDNA; Mouse Receptor 4-1BB protein; H4-1BB protein;
KW human 4-1BB protein; T cell activation; proliferation; immune response;
KW receptor protein; autoimmune disease; organ transplantation;
KW cancerous tumour; nerve growth factor receptor.
XX Mus musculus.
XX WO9936093-A1.
XX 22-JUL-1999.
XX 14-JAN-1999; 99WO-US000823.
XX 14-JAN-1998; 98US-00007097.
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX (KWON/) KWON B S.
XX Kwon BS;
XX WPI; 1999-444325/37.
XX N-PSDB; AAX90763.
XX Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
XX Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.
XX Disclosure; Page 75; 86pp; English.
XX The present sequence is mouse 4-1BB receptor protein. This protein has
XX 65% homology with human receptor protein 4-1BB. The protein has a
XX putative leader sequence, a potential membrane anchor segment and other
XX features of known receptor proteins. 4-1BB is structurally related to
XX members of the nerve growth factor receptor. Probes derived from mouse 4-
XX 1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its
XX ligands, and various monoclonal antibodies have therapeutic uses. They
XX may be used to enhance or suppress T cell activation and proliferation;

CC for activation or inhibition of immune response; to block H4-1BB ligand
 CC binding; treating cancerous tumours and autoimmune diseases; and during
 CC organ transplantation
 XX
 SQ Sequence 256 AA;
 Query Match 100.0%; Score 1428; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.7e-109;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPGTFCKYKVPVCKSCPSTFSSIGGQPN 60
 Db 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPGTFCKYKVPVCKSCPSTFSSIGGQPN 60
 QY 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPGQCTRCCKCRPGQELTKQCKTCS 120
 Db 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPGQCTRCCKCRPGQELTKQCKTCS 120
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVWCGPPVVSFSPSTTISVTPEGPG 180
 Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVWCGPPVVSFSPSTTISVTPEGPG 180
 QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKRPKPHFKOPFKKTTGAAQEDACS 240
 Db 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKRPKPHFKOPFKKTTGAAQEDACS 240
 QY 241 CRCPOEEGGGGGYEL 256
 Db 241 CRCPOEEGGGGGYEL 256

RESULT 6
 AAY33215
 ID AAY33215 standard; protein; 256 AA.
 AC AAY33215;
 DT 18-NOV-1999 (first entry)
 DE Murine CD137 protein.
 XX
 KW CD137; monocyte growth factor; proliferation; peripheral monocyte;
 KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;
 KW immunostimulatory; non-specific immune response; phagocytosis;
 KW intracellular destruction; microorganism; immune complex; antibody;
 KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
 KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
 KW bacterial; viral infection; immunosuppressant; gene therapy; murine.
 XX
 OS Mus sp.
 PN WO9944629-A2.
 XX
 PD 10-SEP-1999.
 XX
 PF 05-MAR-1999; 99WO-EP001440.
 XX
 FR 05-MAR-1998; 98EP-00103859.
 XX
 PA (MERC) MERCKLE GMBH.
 XX
 FI Schwarz H, Langstein J;
 XX
 DR WPI; 1999-550983/46.
 XX
 PT Use of monocyte growth factor CD137 for stimulating proliferation of
 PT peripheral monocytes, particularly for treating immune deficiency, e.g.
 PT following cancer therapy.
 XX
 PS Disclosure; Fig 1B; 57pp; German.
 XX
 CC This invention describes a novel use of the human monocyte growth factor
 CC CD137, or its functional analogs, for (i) stimulating proliferation of

CC peripheral monocytes; and (ii) treating diseases that are associated with
 CC disorders of a cellular system that includes monocytes (and/or their
 CC derived cells, precursor or progenitors) or where the origin and/or
 CC progression is treatable by stimulating proliferation of such cells. The
 CC products of the invention have antitumor, antibacterial, antiviral,
 CC antifungal and immunostimulatory activity. Stimulating proliferation of
 CC monocytes promotes the non-specific immune response, i.e. it increases
 CC phagocytosis and intracellular destruction of microorganisms, immune
 CC complexes and damaged cells, and improves antibody (in)dependent
 CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
 CC diseases associated with a defective immune response where caused by
 CC inadequate numbers of active monocytes/macrophages, especially damage to
 CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation
 CC therapy; disorders of wound healing (e.g. in dialysis or diabetic
 CC patients; or those with chronic venous insufficiency); tumors; bacterial,
 CC fungal or viral infections; (non-)congenital or (non-)inherited diseases
 CC or injury to the immune system; injury induced by treatment with
 CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune
 CC disease, or transplant patients). Nucleic acid encoding (i) can be used
 CC similarly, in gene therapy procedures. Proliferation of peripheral
 CC monocytes is achieved independently of hematopoietic stem cells. This
 CC sequence represents the murine CD137 protein described in the method of
 CC the invention
 XX
 SQ Sequence 256 AA;

Query Match 100.0%; Score 1428; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.7e-109;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPGTFCKYKVPVCKSCPSTFSSIGGQPN 60
 Db 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPGTFCKYKVPVCKSCPSTFSSIGGQPN 60
 QY 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPGQCTRCCKCRPGQELTKQCKTCS 120
 Db 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPGQCTRCCKCRPGQELTKQCKTCS 120
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVWCGPPVVSFSPSTTISVTPEGPG 180
 Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVWCGPPVVSFSPSTTISVTPEGPG 180
 QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKRPKPHFKOPFKKTTGAAQEDACS 240
 Db 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKRPKPHFKOPFKKTTGAAQEDACS 240
 QY 241 CRCPOEEGGGGGYEL 256
 Db 241 CRCPOEEGGGGGYEL 256

RESULT 7
 AAE22581
 ID AAE22581 standard; protein; 256 AA.
 AC AAE22581;
 DT 26-JUL-2002 (first entry)
 XX
 DE Mouse receptore 4-1BB protein.
 XX
 KW Mouse; lymphokine; L2G25B; macrophage inflammatory protein 1 alpha;
 KW MIP-1alpha; immune disease; myeloid progenitor cell differentiation;
 KW 4-1BB; receptor.
 XX
 OS Mus sp.
 XX
 FH Key
 FT Peptide
 FT 1..22
 FT /label= Signal_peptide
 FT 23..256
 FT /note= "Mature receptor 4-1BB protein"
 FT Modified-site 128..130

FT Modified-site /note= "Asn is N-glycosylated"
 FT 138..140
 FT /note= "Asn is N-glycosylated"
 XX US6355476-B1.
 XX 12-MAR-2002.
 XX 30-JUL-1992; 92US-00922996.
 XX 07-NOV-1988; 88US-00267577.
 XX (ADRE-) ADVANCED RES & TECHNOLOGY INC.
 XX Kwon BS, Broxmeyer HE;
 XX WPI; 2002-370577/40.
 XX N-PSDB; AAD35694.
 XX New isolated and purified cDNA designated L25G25B encoding the mouse
 PT lymphokine macrophage inflammatory protein 1 alpha which can be used for
 PT modulating early myeloid progenitor cell differentiation.
 XX Disclosure; Fig 3; 81pp; English.
 XX The invention relates to an isolated and purified cDNA containing mouse
 CC lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage
 CC inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by
 CC which the immune cells communicate with each other. Lymphokines are used
 CC therapeutically against immunologic diseases. Mouse lymphokine MIP-1alpha
 CC can be used to modulate early myeloid progenitor cell differentiation.
 CC The present sequence is mouse lymphokine receptor 4-1BB protein
 XX Sequence 256 AA;
 XX
 Query Match 100.0%; Score 1428; DB 5; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.7e-109;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNVCYVIVVILLVGCERKVGAVQVSCNCPQGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
 Db 1 MGNVCYVIVVILLVGCERKVGAVQVSCNCPQGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
 QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGFGHCLGPQCTCEKDCRPGQELTKQGCKTCS 120
 Db 61 CNICRVAGYFRFKFCSSSTHNAECIEGFGHCLGPQCTCEKDCRPGQELTKQGCKTCS 120
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
 Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
 QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKPFPHIFKQPFKKTGAAQEDACS 240
 Db 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKPFPHIFKQPFKKTGAAQEDACS 240
 QY 241 CRCPQEEGGGGYEL 256
 Db 241 CRCPQEEGGGGYEL 256
 RESULT 8
 ID ABB75954 standard; protein; 256 AA.
 XX ABB75954;
 XX AC
 XX DT 12-JUL-2002 (first entry)
 XX Murine cytokine receptor 4-1BB.
 XX Cytokine; receptor; 4-1BB; mouse.
 XX Mus sp.

XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..256
 FT /label= Mature_protein
 XX US6355779-B1.
 XX 12-MAR-2002.
 XX 10-SEP-1998; 98US-00150864.
 XX 07-MAY-1993; 93US-00060843.
 PR 06-MAY-1994; 94US-00236918.
 PR 05-AUG-1997; 97US-00910449.
 XX (IMMV) IMMUNEX CORP.
 XX Goodwin RG, Smith CA, Alderson MR;
 XX WPI; 2002-380940/41.
 DR N-PSDB; ABL54047.
 XX New antibody specific for the cytokine 4-1BB-ligand, useful for
 PT immunoaffinity purification of the ligand.
 XX Example 1; Col 39-40; 31pp; English.
 CC The present sequence is the protein sequence of the murine cytokine
 CC receptor, 4-1BB. A portion of the extracellular (ligand binding) domain
 CC of the receptor was utilised in a murine 4-1BB/human IgG1 Fc fusion
 CC protein, which was used to identify the murine 4-1BB ligand (4-1BB-L, see
 CC ABB75952). The invention provides novel murine and human 4-1BB-L
 CC polypeptides and human 4-1BB polypeptides, as well as DNA sequences
 CC encoding them, recombinant expression vectors and host cells, and methods
 CC for producing the novel polypeptides by cultivating the transformed host
 CC cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from
 CC their extracellular domains, have therapeutic value. Antibodies that are
 CC immunoreactive with 4-1BB-L or human 4-1BB are claimed
 XX Sequence 256 AA;
 XX
 Query Match 100.0%; Score 1428; DB 5; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.7e-109;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNVCYVIVVILLVGCERKVGAVQVSCNCPQGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
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 QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGFGHCLGPQCTCEKDCRPGQELTKQGCKTCS 120
 Db 61 CNICRVAGYFRFKFCSSSTHNAECIEGFGHCLGPQCTCEKDCRPGQELTKQGCKTCS 120
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
 Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
 QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKPFPHIFKQPFKKTGAAQEDACS 240
 Db 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKPFPHIFKQPFKKTGAAQEDACS 240
 QY 241 CRCPQEEGGGGYEL 256
 Db 241 CRCPQEEGGGGYEL 256
 RESULT 9
 ID ADC25939 standard; protein; 256 AA.
 XX ADC25939;
 XX AC

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XX 18-DEC-2003 (first entry)
XX DT
XX DE Murine receptor 4-1BB protein.
XX AC
XX ADE87549;
XX KW receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;
XX KW cancer; murine; mouse.
XX DE
XX OS Mus musculus.
XX PN US2003100745-A1.
XX PD 29-MAY-2003.
XX PF 04-FEB-2002; 2002US-00067122.
XX PR 07-NOV-1988; 88US-00267577.
XX PR 30-JUL-1992; 92US-00922996.
XX PR 01-FEB-1993; 93US-00012269.
XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX PI Kwon BS;
XX DR WPI; 2003-678138/64.
XX DR N-PSDB; ADC25938.
XX PT New cDNA gene encoding receptor protein 4-1BB, useful for isolating
XX PT similar DNA sequences, and the encoded polypeptide and an antibody to it,
XX PT useful for identifying ligands, and for modulating immune cell activity.
XX PS Claim 7; Fig 2; 77pp; English.
XX CC The invention relates to a novel cDNA gene encoding receptor protein 4-
XX CC 1BB. The cDNA gene of the invention demonstrates immunostimulant
XX CC activities and may be useful as a probe to isolate DNA sequences encoding
XX CC for proteins similar to the receptor protein encoded by the DNA. The
XX CC protein, its fragments and derivatives may be useful as a probe to
XX CC isolate ligands to receptor protein 4-1BB, for stimulating proliferation
XX CC of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand
XX CC binding. The antibody may be useful for enhancing T-cell proliferation or
XX CC activation. Finally, the invention may be useful with respect to cancer
XX CC research. The current sequence is that of the murine receptor 4-1BB
XX CC protein of the invention.
XX SQ Sequence 256 AA;
XX Query Match 100.0%; Score 1428; DB 7; Length 256;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-109;
XX Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNCCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKNPVCKSCPPSTFSSIGQPN 60
Db 1 MGNCCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKNPVCKSCPPSTFSSIGQPN 60
QY 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTCS 120
Db 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
QY 181 GHSIQVLTFLALTSALLALIFITLLFSVLKWKIRKFFPHFKOPFKKTTGAAQEEEDACS 240
Db 181 GHSIQVLTFLALTSALLALIFITLLFSVLKWKIRKFFPHFKOPFKKTTGAAQEEEDACS 240
QY 241 CRCPQEEGGGGYEL 256
Db 241 CRCPQEEGGGGYEL 256

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RESULT 10

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ADE87549
ID ADE87549 standard; protein; 256 AA.
XX AC
XX ADE87549;
XX DT 29-JAN-2004 (first entry)
XX DE Mouse receptor H4-1BB.
XX KW immunosuppressive; H4-1BB ligand binding blocker; mouse;
XX KW receptor protein; H4-1BB; B-cell proliferation stimulator;
XX KW T-cell proliferation enhancer; immune system suppressor; transplantation;
XX KW autoimmune disease.
XX OS Mus sp.
XX PN US2003082157-A1.
XX PD 01-MAY-2003.
XX PF 12-JUN-2002; 2002US-00170997.
XX PR 07-NOV-1988; 88US-00267577.
XX PR 30-JUL-1992; 92US-00922996.
XX PR 01-FEB-1993; 93US-00012269.
XX PR 05-JUN-1995; 95US-00460976.
XX PR 22-OCT-1997; 97US-00955573.
XX PA (KWON/) KWON B S.
XX PI Kwon BS;
XX DR WPI; 2003-576599/54.
XX DR N-PSDB; ADE87548.
XX PT New cDNA, or its encoded receptor protein H4-1BB, useful as probes to
XX PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking
XX PT H4-1BB ligand binding to facilitate organ transplantation or treat
XX PT autoimmune diseases.
XX PS Disclosure; Fig 1; 19pp; English.
XX CC The invention describes a cDNA, which encodes for human receptor protein
XX CC H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe
XX CC to isolate DNA sequences encoding for proteins similar to the receptor
XX CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or
XX CC derivatives, is useful as a probe for identifying ligands to the receptor
XX CC protein H4-1BB, or for stimulating the proliferation of B-cells
XX CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are
XX CC useful for enhancing T-cell proliferation of activation. The cDNA or
XX CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand
XX CC binding, which is particularly useful for suppressing the immune system
XX CC during transplantation, or for treating autoimmune diseases. This is the
XX CC amino acid sequence of mouse receptor H4-1BB.
XX SQ Sequence 256 AA;
XX Query Match 100.0%; Score 1428; DB 7; Length 256;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-109;
XX Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNCCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKNPVCKSCPPSTFSSIGQPN 60
Db 1 MGNCCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKNPVCKSCPPSTFSSIGQPN 60
QY 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTCS 120
Db 61 CNICRVACGYFRFKFCSSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180

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1 MGNNCYNVWVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNFVKSCPPSTFSSIGGQPN 60

61 CNICRVCAGYFRFKKFCSSSTHNAECECEIEGFHCLGPGQCTRCEKDCRPGQELTKQGCKTCS 120

100

[illegible]

RESULT 12

AA64197;

[illegible]

Homo sapiens.

24-NOV-1994.

07-MAY-1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680,

XX

CTC
Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB

IL-1 β and IL-18 (proinflammatory cytokines) and the 4-1BB-L (cytokine receptor) see AA075423)

mechanisms of T-cell activation, as they are expressed on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation

Человек не может жить без общения. Он нуждается в общении с другими людьми, с природой, с самим собой. Общение — это процесс взаимодействия, который позволяет человеку реализовать свои потребности, раскрыть свои способности, достичь своих целей. Общение — это искусство, которое требует практики, терпения и уважения к другим людям. Общение — это мост, который соединяет людей, делает их ближе друг к другу, помогает им преодолевать трудности, делиться опытом, поддерживать друг друга. Общение — это основа жизни, без которой человек не может существовать. Общение — это дар, который мы получаем от природы, и который мы должны использовать мудро, чтобы сделать нашу жизнь более полной, интересной и有意义.

Best Local Similarity 58.4%; Pred. No. 2.1e-57;

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QY 60 NNCICRVAGYFRFKKFCSTNAECIEGPHCLGPQCTRCCKCRPGQELTKGCKTC 119
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QY 120 SLGTENDONGTGVCRPTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKIRKFPFHIFKQPFKKTGAAQE 235
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLFTLAFSVVVKGRKLLYIFKQPFVRPVQTTQE 237
QY 236 EDACSCRCPOEBEGG 250
Db 238 EDGCSRCRFPPEEBEGG 252

RESULT 13
AAR70977
ID AAR70977 standard; protein; 255 AA.
XX AC AAR70977;
XX DT 25-MAR-2003 (revised)
XX DT 16-OCT-1995 (first entry)
XX DE H4-1BB receptor protein.
XX KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
XX KW organ transplantation; cell membrane ligand.
XX OS Homo sapiens.
XX PN WO9507984-A1.
XX PD 23-MAR-1995.
XX PF 15-SEP-1994; 94WO-US010457.
XX PR 16-SEP-1993; 93US-00122796.
XX PA (INDV ) UNIV INDIANA FOUND.
XX PI Kwon BS;
XX DR WPI; 1995-131352/17.
XX DR N-PSDB; AAQ86126.
XX PT Novel cDNA encoding human receptor protein H4-1BB - useful to produce the
XX PT protein which is used to treat autoimmune disease and facilitate organ
XX PT transplantation.
XX PS Claim 6; Fig 2; 36pp; English.
XX CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using
XX CC probes based on the mouse receptor protein 4-1BB gene. The PCR product
XX CC was used to screen a cDNA library of activated human T-cells. The
XX CC isolated cDNA (AAQ86126), deposited as NRRL AAB21131, encoded the human
XX CC homolog, H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct
XX CC PN field.)
XX SQ Sequence 255 AA;
Query Match 55.7%; Score 795; DB 2; Length 255;
Best Local Similarity 58.4%; Pred. No. 2.1e-57;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNKCYNNVIVILLVCGEKVAVQNSCDNCPQGTTC-RXNYPVCXSCPTSFSSIGGGP 59
Db 1 MGNKCYNNVIVATLLVLNFERLSLDQPCNCPAGTCDNNRNGICFCPPNSFSAGGOR 60
QY 60 NNCICRVAGYFRFKKFCSTNAECIEGPHCLGPQCTRCCKCRPGQELTKGCKTC 119

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Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHLGAGCSMCEQDCKQOGLTKGCKDC 120
QY 120 SLGTENDONGTGVCRPTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKIRKFPFHIFKQPFKKTGAAQE 235
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLFTLAFSVVVKGRKLLYIFKQPFVRPVQTTQE 237
QY 236 EDACSCRCPOEBEGG 250
Db 238 EDGCSRCRFPPEEBEGG 252

RESULT 14
AAW26658
ID AAW26658 standard; protein; 255 AA.
XX AC AAW26658;
XX DT 25-MAR-2003 (revised)
XX DT 25-FEB-1998 (first entry)
XX DE Human 4-1BB receptor.
XX KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte; T cell;
XX KW proliferation; immunostimulant.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT /label= Sig_peptide
XX FT Domain
XX FT /label= Cytoplasmic
XX FT Modified-site
XX FT /note= "Asn is N-glycosylated"
XX FT Modified-site
XX FT /note= "Asn is N-glycosylated"
XX FT Domain
XX FT /label= Transmembrane
XX FT Domain
XX FT /label= Extracellular
XX PN US5674704-A.
XX PD 07-OCT-1997.
XX PF 06-MAY-1994; 94US-00236918.
XX PR 07-MAY-1993; 93US-00060843.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Alderson MR, Goodwin RG, Smith CA;
XX WPI; 1997-502333/46.
XX DR N-PSDB; AAT91026.
XX PT DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell
XX PT proliferation in vitro, and as research tools.
XX PS Example 2; Col 43-44; 32pp; English.
XX CC This protein comprises human 4-1BB, a member of the tumour necrosis
XX CC factor receptor superfamily that is expressed on cells that include, but
XX CC are not limited to, stimulated human peripheral blood lymphocytes. Its
XX CC amino acid sequence was deduced from an isolated cDNA clone (see
XX CC AAT91026) obtained from human peripheral blood T-lymphocytes. A novel
XX CC claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified,
XX CC cloned and sequenced (see AAW26657) that binds to 4-1BB. 4-1BB-L,

```

CC especially its soluble extracellular domain, can be used to stimulate T-
CC cell proliferation in vitro, as a research tool and as an affinity ligand
CC for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX
SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 2; Length 255;
Best Local Similarity 58.4%; Pred. No. 2.1e-57;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSPPTFSIGGQP 59
DB 1 MGNVCNVIVATLLVNLNFERTRSLQDPCSNCPAGTFCDDNNRNIQCSPPNPSFSSAGGQR 60
QY 60 NCNCRVACGYPRFKKFCSTHNAECIEGHCILGPOCTRCCKRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKSCSTNAECDCCTPGFHCILGAGCSMCQDCKQGLTKGCKDC 120
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVWFSPTTISVTPEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSFGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPHIFKOPFKTTGAQE 235
DB 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEGG 250
DB 238 EDGCSRCRFPPEEEGG 252

RESULT 15
AAV28688
ID AAY28688 standard; protein; 255 AA.
AC AAY28688;
XX
XX
DT 13-OCT-1999 (first entry)
DE Human receptor protein 4-1BB.

XX Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation;
KW mouse 4-1BB cDNA; monoclonal antibody; immune response;
KW organ transplantation; autoimmune disease; diabetes; cancerous tumour;
KW rheumatoid arthritis; lupus; nerve growth factor receptor.
XX
XX Homo sapiens.

OS Key Location/Qualifiers
FH Protein 18..255
FT /note= "Purified human 4-1BB"
FT
XX
XX W09936093-A1.
XX 22-JUL-1999.
XX
XX 14-JAN-1999; 99WO-US000823.
XX
XX 14-JAN-1998; 98US-00007097.
XX
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA (KWON/) KWON B S.
XX
XX Kwon BS;
XX
XX WPI; 1999-444325/37.
DR N-PSDB; AAZ08961.
XX
XX Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.
XX
XX Claim 4; Page 77-78; 86pp; English.

CC The present sequence is a human receptor protein 4-1BB. 4-1BB is
CC structurally related to members of the nerve growth factor receptor. It
CC contains a putative zinc finger structure similar to that of yeast eIF-2b
CC protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of
CC H4-1BB. The H4-1BB protein, its ligands, and various monoclonal
CC antibodies have therapeutic uses. They may be used to enhance or suppress
CC T cell activation and proliferation; B cell proliferation; treating
CC cancerous tumours and AIDS. The use of H4-1BB to block H4-1BB ligand
CC binding has practical application in the suppression of immune system
CC during organ transplantation or against autoimmune diseases including
CC diabetes, rheumatoid arthritis, and lupus
XX
XX SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 2; Length 255;
Best Local Similarity 58.4%; Pred. No. 2.1e-57;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSPPTFSIGGQP 59
DB 1 MGNVCNVIVATLLVNLNFERTRSLQDPCSNCPAGTFCDDNNRNIQCSPPNPSFSSAGGQR 60
QY 60 NCNCRVACGYPRFKKFCSTHNAECIEGHCILGPOCTRCCKRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKSCSTNAECDCCTPGFHCILGAGCSMCQDCKQGLTKGCKDC 120
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVWFSPTTISVTPEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSFGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPHIFKOPFKTTGAQE 235
DB 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEGG 250
DB 238 EDGCSRCRFPPEEEGG 252

RESULT 16
AAV33214
ID AAY33214 standard; protein; 255 AA.
XX
XX AC AAY33214;
XX
XX DT 18-NOV-1999 (first entry)
XX
XX Human CD137 protein.
XX
XX CD137; monocyte growth factor; proliferation; peripheral monocyte;
KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;
KW immunostimulatory; non-specific immune response; phagocytosis;
KW intracellular destruction; microorganism; immune complex; antibody;
KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
KW bacterial; viral infection; immunosuppressant; gene therapy; human.
XX
XX Homo sapiens.
XX
XX W09944629-A2.
XX
XX 10-SEP-1999.
XX
XX 05-MAR-1999; 99WO-EP001440.
XX
XX 05-MAR-1998; 98EP-00103859.
XX
XX (MERC) MERCKLE GMBH.
XX
XX Schwarz H, Langstein J;
XX WPI; 1999-550993/46.
DR N-PSDB; AAZ09769.

XX Use of monocyte growth factor CD137 for stimulating proliferation of
 PT peripheral monocytes, particularly for treating immune deficiency, e.g.
 PT following cancer therapy.
 XX
 XX
 PS Claim 12; Fig 1A; 57pp; German.
 XX
 CC This invention describes a novel use of the human monocyte growth factor
 CC CD137, or its functional analogs, for (i) stimulating proliferation of
 CC peripheral monocytes; and (ii) treating diseases that are associated with
 CC disorders of a cellular system that includes monocytes (and/or their
 CC derived cells, precursor or progenitors) or where the origin and/or
 CC progression is treatable by stimulating proliferation of such cells. The
 CC products of the invention have antitumor, antibacterial, antiviral,
 CC antifungal and immunostimulatory activity. Stimulating proliferation of
 CC monocytes promotes the non-specific immune response, i.e. it increases
 CC phagocytosis and intracellular destruction of microorganisms, immune
 CC complexes and damaged cells, and improves antibody (in) dependent
 CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
 CC diseases associated with a defective immune response where caused by
 CC inadequate numbers of active monocytes/macrophages, especially damage to
 CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation
 CC therapy; disorders of wound healing (e.g. in dialysis or diabetic
 CC patients, or those with chronic venous insufficiency); tumors; bacterial,
 CC fungal or viral infections; (non-)congenital or (non-)inherited diseases
 CC or injury to the immune system; injury induced by treatment with
 CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune
 CC disease, or transplant patients). Nucleic acid encoding (I) can be used
 CC similarly, in gene therapy procedures. Proliferation of peripheral
 CC monocytes is achieved independently of hematopoietic stem cells. This
 CC sequence represents the human CD137 protein described in the method of
 CC the invention
 XX

Sequence 255 AA;

Query Match 55.7%; Score 795; DB 2; Length 255;
 Best Local Similarity 58.4%; Pred. No. 2.1e-57;
 Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
 QY 1 MGNNCYNVVWVILLVGCCKVAVQNSCDNCPQGTFC-RKYNPVCKSCPSTSSIGQP 59
 Db 1 MGNSCYNIVALLVAVLAFRTSRSLQDPCSNCPAGTFCDNRRNQICSPNPSFSSAGQR 60
 QY 60 NCNTRVCAGYFRPKKFCSSSTHNAECBIEGFHCLGPGQCTCEKDCRPGQELTKQGKTC 119
 Db 61 TCDICRQCKGVFRTRKECSSTNSAECDCPTGFHCLGAGCSMCEQDCQGGELTKGCKDC 120
 QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTISVTPGGP 179
 Db 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLVNGTKERDVVCGPSPADLSFGAS-SVTPP-AP 177
 QY 180 G---GHSLOVLTFLAULTS-ALLALIFITLFSVLKWKRPKPFKKTGTAAQE 235
 Db 178 AREPCHSPQIISFLAULTSALLFLFLTLRFSVVRGKRLLYIFKQPFMPVQTQE 237
 QY 236 EDACSCRCPOEEGG 250
 Db 238 EDGSCRCFPPEEGG 252
 RESULT 17
 AAEE08546
 ID AA08546 standard; protein; 255 AA.
 XX
 AC AA08546;
 XX
 DT 15-NOV-2001 (first entry)
 XX Human h4-1BB receptor.
 DE
 XX Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;
 KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;
 KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;
 KW

KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;
 KW bone resorption; human immunodeficiency virus; HIV; graft rejection;
 KW inflammation; antibacterial; immunosuppressive; vulvectomy; vasotropic;
 KW antiinflammatory; protozoicide; cachexia; immunomodulator; virucide.
 XX
 OS Homo sapiens.
 XX
 PN US2001014465-A1.
 XX
 PD 16-AUG-2001.
 XX
 PF 19-DEC-2000; 2000US-00739394.
 XX
 PR 15-MAR-1996; 96US-0013474P.
 PR 13-MAR-1997; 97US-00816605.
 PR 22-FEB-1999; 99US-00253549.
 XX
 PA (NIJU/) NI J.
 PA (YUGG/) YU G.
 PA (GENT/) GENTZ R.
 PA (DILL/) DILLON P. J.
 XX
 PI Ni J, Yu G, Gentz R, Dillon PJ;
 XX WPI; 2001-529104/58.
 XX
 PT New human 4-1BB receptor splicing variant polypeptides and
 PT polynucleotides, useful for research, diagnosis, prevention and treatment
 PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
 PT syndrome and graft rejection.
 XX
 PS Disclosure; Fig 2; 28pp; English.
 XX
 CC The present invention relates to an isolated human 4-1BB receptor
 CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
 CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
 CC gene therapy. h4-1BBSV is useful for research, biological, clinical and
 CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives
 CC are useful as an immunogen to produce antibodies which are useful for
 CC isolating and identifying clones expressing the polypeptide or to purify
 CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of
 CC disorders of cells, tissues and organisms and its nucleic acid is useful
 CC for detecting complementary polynucleotides for e.g. as a diagnostic
 CC reagent and for chromosomal identification. h4-1BBSV receptor agonists
 CC are useful for preventing, treating tumours, restenosis, cytotoxicity,
 CC bacterial and viral infection, deleterious effects of ionising radiation,
 CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-
 CC host rejection, to regulate immune responses, wound healing and cellular
 CC proliferation and antagonists are useful for treating and/or preventing
 CC endotoxin shock, inflammation, cerebral malaria, activation of human
 CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
 CC cachexia. The present sequence is human h4-1BB receptor
 XX

Sequence 255 AA;

Query Match 55.7%; Score 795; DB 4; Length 255;
 Best Local Similarity 58.4%; Pred. No. 2.1e-57;
 Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
 QY 1 MGNNCYNVVWVILLVGCCKVAVQNSCDNCPQGTFC-RKYNPVCKSCPSTSSIGQP 59
 Db 1 MGNSCYNIVALLVAVLAFRTSRSLQDPCSNCPAGTFCDNRRNQICSPNPSFSSAGQR 60
 QY 60 NCNTRVCAGYFRPKKFCSSSTHNAECBIEGFHCLGPGQCTCEKDCRPGQELTKQGKTC 119
 Db 61 TCDICRQCKGVFRTRKECSSTNSAECDCPTGFHCLGAGCSMCEQDCQGGELTKGCKDC 120
 QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTISVTPGGP 179
 Db 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLVNGTKERDVVCGPSPADLSFGAS-SVTPP-AP 177
 QY 180 G---GHSLOVLTFLAULTS-ALLALIFITLFSVLKWKRPKPFKKTGTAAQE 235
 Db 178 AREPCHSPQIISFLAULTSALLFLFLTLRFSVVRGKRLLYIFKQPFMPVQTQE 237
 QY 236 EDACSCRCPOEEGG 250
 Db 238 EDGSCRCFPPEEGG 252

Db 178 AREPHGSPQIIFFFLALTGTALLFLFLFLTLRFSVVGRKKLLYFKQPMRPVQTTOE 237

QY 236 EDACSCRCPEEEGG 250

Db 238 EDGSCRCFPEEEGG 252

RESULT 18

AAB50521

ID AAB50521 standard; protein; 255 AA.

XX

AC AAB50521;

XX

DT 15-MAR-2001 (first entry)

XX

DE Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.

XX

KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neutrotropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotrophic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticongulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.

XX

OS Homo sapiens.

XX

PN WC200071150-A1.

XX

PD 30-NOV-2000.

XX

PF 18-MAY-2000; 2000WO-US013515.

XX

PR 20-MAY-1999; 99US-0135164P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Wei Y, Ruben SM, Gentz RL, Ni J;

XX

DR WPT; 2001-041051/05.

XX

XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.

XX

PS Disclosure; Fig 2; 285pp; English.

XX

CC The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, neutrotropic, neuroprotective, antiviral, antiinflammatory, anticongulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotrophic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present invention represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention

XX

SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 4; Length 255;

Best Local Similarity 59.4%; Pred. No. 2.1e-57;

Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVIVLLVGCERKVGAVONSCDNCQPGTFC-RKYNPVCKSPSTSSIGGQP 59

Db 1 MGNVCYVIVATLLVLFNFTSLQDFCSNCPAGTFCDDNRNQCPCPPNPSAGQR 60

QY 60 NCNCRVCAGYFRPKFCSTHNAECIEGFHCLGQCTRCCEKDCRPGQELTRQCKTC 119

Db 61 TCDICRQCKGVFRTRKECSSISNAECDCCTFGFHLGAGCSNCEQDCQGOELTKGCKDC 120

QY 120 SLGTFNDQNGTGVCRPWTNCSLDGORSVLKGTGTTKDVWCGPPVVSFSPSTISVTPEGGP 179

Db 121 CFGTFNDOK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSFGAS-SVTTP-AP 177

QY 180 G---CHSLQVLTFLALTS-ALLLALIFITLLFSLVKWIRKKFPHIFKQPFKTTGAAQE 235

Db 178 AREPHGSPQIIFFFLALTGTALLFLFLFLTLRFSVVGRKKLLYFKQPMRPVQTTOE 237

QY 236 EDACSCRCPEEEGG 250

Db 238 EDGSCRCFPEEEGG 252

RESULT 19

AAB75955

ID AAB75955 standard; protein; 255 AA.

XX

AC AAB75955;

XX

DT 12-JUL-2002 (first entry)

XX

DE Human cytokine receptor 4-1BB.

XX

KW Cytokine; receptor; 4-1BB; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..23 /label= Signal_peptide

FT Protein 24..255 /label= Mature_protein

FT Domain 24..186 /note= "extracellular domain"

FT Modified-site 138..140 /note= "Asn is N-glycosylated"

FT Modified-site 149..151 /note= "Asn is N-glycosylated"

FT Region 186..213 /note= "transmembrane region"

FT Domain 214..255 /note= "cytoplasmic domain"

XX

XX US6355779-B1.

PN 12-MAR-2002.

XX

PD 10-SEP-1998; 98US-00150864.

XX

XX 07-MAY-1993; 93US-00060843.

PR 06-MAY-1994; 94US-00236918.

PR 05-AUG-1997; 97US-00910449.

XX

PA (IMV) IMMUNEX CORP.

XX

XX Goodwin RG, Smith CA, Alderson MR;

XX

DR WPI; 2002-380940/41.

DR N-PSDB; ABL54048.

XX

FT New antibody specific for the cytokine 4-1BB-ligand, useful for

PT immunofluorescence purification of the ligand.

PS Example 2; Col 43-44; 31pp; English.

XX The present sequence is the protein sequence of the human cytokine
CC receptor, 4-1BB. The sequence was deduced from a cDNA clone (see
CC ABL54048) obtained from a human peripheral blood T-lymphocyte cDNA
CC library. It shows 60% identity to murine 4-1BB (see ABB75954). A portion
CC of the extracellular (ligand binding) domain of the human 4-1BB cytokine
CC receptor was used to identify the human 4-1BB/IG1 Fc fusion protein.
CC which was used to identify the human 4-1BB ligand (4-1BB-L, see
CC ABB75953). The invention provides novel murine and human 4-1BB-L
CC polypeptides and human 4-1BB polypeptides, as well as DNA sequences
CC encoding them, recombinant expression vectors and host cells, and methods
CC for producing the novel polypeptides by culturing the transformed host
CC cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from
CC their extracellular domains, have therapeutic value. Antibodies that are
CC immunoreactive with 4-1BB-L or human 4-1BB are claimed

XX Sequence 255 AA;

Query Match 55.7%; Score 795; DB 5; Length 255;
Best Local Similarity 58.4%; Pred. No. 2.1e-57;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNNVNVVVVILLVGGCKGAVQNSDNCOPGTFRC-RKYNPVCKSPSTFSSIGQP 59
DB 1 MGNSCVNIVATLLVNFRTSLQDPCSNCPAGTFCNNRNQICSPCPNPSFSSAGQR 60
QY 60 NCNCRVAGYFRFKFCSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKESSTSNABCDCTPGPHCLGAGCSNCEQDCKQQLTKGCKDC 120
QY 120 SLGTENDONGTGVCRPTWNCSDGSLVLTGTETKDVVCGPVVFSFSTISVTPBGGP 179
DB 121 CFGTENDQK-RGICRPWNCSDGSLVLTGTETKDVVCGPVVFSFSTISVTPBGGP 177
QY 180 G---GHSIQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTITGAQE 235
DB 178 AREPGHSPQIISFFLALTSALLFLFLFLLTFLRFSVWKGKLLVIFKQPMRPVQITQE 237
QY 236 EDACSCRCPOEEGG 250
DB 238 EDGCSRCRPEEEGG 252

RESULT 20
ABR39863
ID ABR39863 standard; protein; 255 AA.
XX ABR39863;
AC ABR39863;
XX 11-AUG-2003 (first entry)
DE Human MOCEPTIN polypeptide.
KW MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic;
KW antilipemic; antiarteriosclerotic; antidiabetic; cerebroprotective;
KW hypotensive; immunomodulator; antidepressant; human; receptor.
OS Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..17
FT Protein /note= "putative signal peptide"
FT Protein /note= "mature protein"
FT Domain /note= "extracellular domain"
FT Domain /note= "transmembrane domain"
FT Domain 214..255

XX WO2003011325-A1.
XX 13-FEB-2003.
XX 25-JUL-2002; 2002WO-IB003499.
XX 27-JUL-2001; 2001US-0308142P.
XX (GBST) GENSET SA.
XX Lucas J, Dialynas D, Briggs K;
XX WPT; 2003-268084/26.
XX N-PSDB; ACC47324.
XX New agonist and antagonist of MOCEPTIN (a member of the Tumor Necrosis
XX Factor Receptor family) activity, useful for preventing or treating
XX obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing
XX body mass.
XX Disclosure; Page 32-33; 37pp; English.
XX The invention relates to an agonist or antagonist of MOCEPTIN (a member
XX of the Tumour Necrosis Factor Receptor family) activity. The antagonist
XX or agonist of MOCEPTIN activity, or the composition comprising the
XX agonist or antagonist, is useful for preventing or treating an obesity-
XX related disorder or disease in an individual. In particular, the agonist
XX of MOCEPTIN activity is useful for treating or preventing obesity-related
XX diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance,
XX diabetes, stroke or hypertension. The agonist is also useful for reducing
XX body mass and maintaining weight loss. The antagonist of MOCEPTIN
XX activity is useful for increasing body mass, or for treating or
XX preventing disorders associated with excessive weight loss, e.g.
XX cachexia, cancer-related weight loss, AIDS-related weight loss, chronic
XX inflammatory disease-related weight loss, or anorexia. The present
XX sequence represents a human MOCEPTIN polypeptide
XX Sequence 255 AA;

Query Match 55.7%; Score 795; DB 6; Length 255;
Best Local Similarity 58.4%; Pred. No. 2.1e-57;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNNVNVVVVILLVGGCKGAVQNSDNCOPGTFRC-RKYNPVCKSPSTFSSIGQP 59
DB 1 MGNSCVNIVATLLVNFRTSLQDPCSNCPAGTFCNNRNQICSPCPNPSFSSAGQR 60
QY 60 NCNCRVAGYFRFKFCSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKESSTSNABCDCTPGPHCLGAGCSNCEQDCKQQLTKGCKDC 120
QY 120 SLGTENDONGTGVCRPTWNCSDGSLVLTGTETKDVVCGPVVFSFSTISVTPBGGP 179
DB 121 CFGTENDQK-RGICRPWNCSDGSLVLTGTETKDVVCGPVVFSFSTISVTPBGGP 177
QY 180 G---GHSIQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTITGAQE 235
DB 178 AREPGHSPQIISFFLALTSALLFLFLFLLTFLRFSVWKGKLLVIFKQPMRPVQITQE 237
QY 236 EDACSCRCPOEEGG 250
DB 238 EDGCSRCRPEEEGG 252

RESULT 21
ABB84640
ID ABB84640 standard; protein; 255 AA.
XX ABB84640;
AC ABB84640;
XX 05-FEB-2003 (first entry)
DT

DE XX Human h4-1BB receptor.

KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;

KW anti-HIV; antibacterial; anti-inflammatory; protozoacide; immunomodulator;

KW vasotropic; gene therapy; chromosome mapping; extracellular domain;

KW endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease;

KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;

KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;

KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;

KW autoimmune disease; h4-1BB.

OS XX Homo sapiens.

PN XX US2002127651-A1.

XX 12-SEP-2002.

XX 15-MAR-2002; 2002US-00097330.

XX 15-MAR-1996; 96US-0013474P.

PR 13-MAR-1997; 97US-00816605.

PR 22-FEB-1999; 99US-00253549.

PR 19-DEC-2000; 2000US-00739394.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Gentz RL, Dillon PJ;

XX WPI; 2003-066900/06.

XX Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,

PT providing resistance to bacteria, viruses and parasites, to induce

PT proliferation of endothelial cells, and to treat restenosis.

XX Disclosure; Fig 2; 29pp; English.

XX This invention describes a novel human h4-1BBSV receptor or a sequence

CC that is at least 85% identical to the h4-1BBSV receptor. The product of

CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,

CC antibacterial, anti-inflammatory, protozoacide, immunomodulator and

CC vasotropic activity and can be used for gene therapy and chromosome

CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to

CC a disease related to underexpression of h4-1BBSV or for identifying

CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV

CC receptor polypeptide is useful for treating and/or preventing endotoxic

CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human

CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or

CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired

CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,

CC viruses and parasites, to induce proliferation of endothelial cells and

CC certain haematopoietic cells, to treat restenosis and to prevent certain

CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.

CC This sequence represents the human 4-1BB receptor described in the

CC disclosure of the invention

XX XX

SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 6; Length 255;

Best Local Similarity 58.4%; Pred. No. 2.1e-57;

Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVNVVIVLLVGGCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGQP 59

DB 1 MGNVNVVIVATLLVILNFERTRSLQDFCSNCPAGTFCDNNRNQICSPCPNFSFSSAGGQR 60

QY 60 NCNCRVCAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDRPGQELTKQGCKTC 119

DB 61 TCDICRCKGVFRTRKECSSTSNACEDCTPGFHCLGAGCSMCEQDKQGGELTKGCKOC 120

QY 120 SLGTFNDONGTGVCRPWTNCSLDGSRVLTGTTIEKDVVCGPPVVSFSPSTTISVTEGGP 179

DB 121 CFTGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGFSPADLSPGAS-SVTPP-AP 177

QY 180 G---GHSLQVLTFLALTS-ALLIALIFITLLFSVLKWKIRKPFHIFKPFKKTGAQE 235

DB 178 AREFGHSPQIISFALATSTALLFLFFLTFRSVVGRKLLYIFKQPFMRPVQTQE 237

QY 236 EDACSCRCPOEEGG 250

DB 238 EDGSCRFPEEEGG 252

RESULT 22

AAE39531

ID AAE39531 standard; protein; 255 AA.

XX AAE39531;

XX 18-DEC-2003 (first entry)

XX Human protein SEQ ID NO: 2.

XX Human; adhesive; packaging.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 107

FT /note= "Encoded by AGA"

XX US2003000851-A1.

XX 02-JAN-2003.

XX 08-JUN-2001; 2001US-00877336.

XX 08-JUN-2001; 2001US-00877336.

XX (WALS/) WALSH J C.

XX (HAWK/) HAWKINS K E.

XX Walsh JC, Hawkins KE;

XX WPI; 2003-266968/26.

XX N-PSDB; AAD59981.

XX Paper board container manufacture for soap boxes, involves applying

PT adhesive on blank while moving in one direction, which is folded, and

PT then another quantity of adhesive is applied before moving blank to

PT another direction.

XX Disclosure; Page 12-13; 46pp; English.

XX The invention relates to a method and apparatus for applying adhesive to

CC packaging in a variety of configurations. The method involves applying

CC adhesive on blank while moving in one direction, which is folded, and

CC then another quantity of adhesive is applied before moving blank to

CC another direction. The invention is useful for e.g. soap boxes, cereal

CC boxes, bottle carriers, can boxes. The present sequence is human protein.

CC Note: there is no specific information about the sequence in the

CC specification

XX XX

SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 7; Length 255;

Best Local Similarity 58.4%; Pred. No. 2.1e-57;

Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVNVVIVLLVGGCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGQP 59

DB 1 MGNVNVVIVATLLVILNFERTRSLQDFCSNCPAGTFCDNNRNQICSPCPNFSFSSAGGQR 60

QY 60 NCNCRVCAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDRPGQELTKQGCKTC 119

DB 61 TCDICRCKGVFRTRKECSSTSNACEDCTPGFHCLGAGCSMCEQDKQGGELTKGCKDC 120

QY 120 SLGTNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPVPVVSFSPTTISVTPEGP 179
 DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGSPADLSPGAS-SVTTP-AP 177
 QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWKIRKFPFHIFKOPFKKTTGAAOE 235
 DB 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKGRKKLLYIFKOPFMRPVQTTQE 237

QY 236 EDACRCRQPEEGG 250
 DB 238 EDGCSRFPPEEGG 252

RESULT 23

ADC78803
 ID ADC78803 standard; protein; 255 AA.

AC ADC78803;

DT 01-JAN-2004 (first entry)

DE Human PRO protein #16.

XX human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease.

XX Homo sapiens.

XX WO2003034984-A2.

XX 01-MAY-2003.

PF 15-OCT-2002; 2002WO-US033070.

PR 19-OCT-2001; 2001US-0340083P.

XX (GETH) GENENTECH INC.

PI Goddard A, Gurney AL;

DR WPI: 2003-481990/45.

DR N-PSDB; ADC78802.

XX New PRO polynucleotide and polypeptide, useful for the manufacture of a
 PT medicament for diagnosing or treating cancer or inflammatory bowel
 PT disorder e.g., ulcerative colitis or Crohn's disease.

XX Claim 12; SEQ ID NO 32; 327pp; English.

XX The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for
 CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

XX Sequence 255 AA;

Query Match 55.7%; Score 795; DB 7; Length 255;
 Best Local Similarity 58.4%; Pred. No. 2.1e-57;
 Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MNNCYNIVVLLVAVGCEKVGAVQNSCDNCPQTFRC-RKYNPVCKSCPSTSSITGGQP 59

DB 1 MNSCYNIVATLLVLAIFERTSRSLQDPCSNCPAGTFCDNNRNQICSPCPNPSFSSAGGQR 60

QY 60 NCNCRVAGYFRPKFCSSFHNAECBIEGFHCLGPQCTRCBKDCRPGQELTKQGCKTC 119

DB 61 TCDICRQCKGVFRTRKECSSTFNAECDCTFGHCLGAGCSWCBQDCKQGQELTKGCKDC 120

QY 120 SLGTNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPVPVVSFSPTTISVTPEGP 179

DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGSPADLSPGAS-SVTTP-AP 177

QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWKIRKFPFHIFKOPFKKTTGAAOE 235
 DB 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKGRKKLLYIFKOPFMRPVQTTQE 237
 QY 236 EDACRCRQPEEGG 250
 DB 238 EDGCSRFPPEEGG 252

RESULT 24

ADD25599

ID ADD25599 standard; protein; 255 AA.

XX AC ADD25599;

XX DT 15-JAN-2004 (first entry)

XX Binding domain-immunoglobulin fusion protein-associated protein #77.

XX Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type 1 diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

XX US2003118592-A1.

XX 26-JUN-2003.

XX 25-JUL-2002; 2002US-00207655.

XX 17-JAN-2001; 2001US-0367358P.

XX 17-JAN-2002; 2002US-00053530.

XX 03-JUN-2002; 2002US-0385691P.

XX (GENE-) GENE-CRAFT INC.

XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 WPI: 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX Disclosure; SEQ ID NO 160; 157pp; English.
 XX The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an

CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide operably linked to a promoter,
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=2003018592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID
 CC number therefore none of the sequences can be explicitly identified.
 XX
 SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 7; Length 255;
 Best Local Similarity 58.4%; Pred. No. 2.1e-57;
 Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVNVVILLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 59
 DB 1 MGNVCYVNVVILLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 60

QY 60 NCNCRVCAGYFRFKFCSTHNAECIEGFGHCLGPOCTCEKDCRQBELTKGCKTC 119
 DB 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGGCMCEQDCKQBELTKGCKDC 120

QY 120 SLGTENDQNGTVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVWSPSPSTTISVTPEGGP 179
 DB 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLVNGTKERDVVCGPSPADLSPGAS-SVTTPP-AP 177

QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHIFKQPFKTTGAQE 235
 DB 178 AREPGHSPQIISFFLALTSTALLFLPFLTLRFSVWKGKRLLYIFKQPFMRPVQTQOE 237

QY 236 EDACSCRCPOEEGG 250
 DB 238 EDGCSRFPPEEEGG 252

RESULT 25
 AD887541
 ID ADE87541 standard; protein; 255 AA.
 AC ADE87541;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Unknown human receptor H4-1BB.
 XX
 XX immunosuppressive; H4-1BB ligand binding blocker; human;
 KW receptor protein; H4-1BB; B-cell proliferation stimulator;
 KW T-cell proliferation enhancer; immune system suppressor; transplantation;
 KW autoimmune disease.
 XX
 OS Homo sapiens.
 XX
 XX US2003082157-A1.
 XX
 XX 01-MAY-2003.
 XX
 XX 12-JUN-2002; 2002US-00170997.
 XX
 XX 07-NOV-1988; 88US-00267577.
 PR 30-JUL-1992; 92US-00922996.
 PR 01-FEB-1993; 93US-00012269.
 PR

PR 05-JUN-1995; 95US-00460976.
 XX 22-OCT-1997; 97US-00955573.
 PA (KWON)/ KWON B S.
 XX Kwon BS;
 XX WPI: 2003-576599/54.
 DR N-PSDB; ADE87540.
 XX
 XX New cDNA, or its encoded receptor protein H4-1BB, useful as probes to
 PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking
 PT H4-1BB ligand binding to facilitate organ transplantation or treat
 PT autoimmune diseases.
 XX
 PS Disclosure; SEQ ID NO 2; 19pp; English.
 XX
 CC The invention describes a cDNA, which encodes for human receptor protein
 CC H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe
 CC to isolate DNA sequences encoding for proteins similar to the receptor
 CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or
 CC derivatives, is useful as a probe for identifying ligands to the receptor
 CC protein H4-1BB, or for stimulating the proliferation of B-cells
 CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are
 CC useful for enhancing T-cell proliferation of activation. The cDNA or
 CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand
 CC binding, which is particularly useful for suppressing the immune system
 CC during transplantation, or for treating autoimmune diseases. This is the
 CC amino acid sequence of unknown human receptor H4-1BB.
 XX
 SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 7; Length 255;
 Best Local Similarity 58.4%; Pred. No. 2.1e-57;
 Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVNVVILLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 59
 DB 1 MGNVCYVNVVILLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 60

QY 60 NCNCRVCAGYFRFKFCSTHNAECIEGFGHCLGPOCTCEKDCRQBELTKGCKTC 119
 DB 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGGCMCEQDCKQBELTKGCKDC 120

QY 120 SLGTENDQNGTVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVWSPSPSTTISVTPEGGP 179
 DB 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLVNGTKERDVVCGPSPADLSPGAS-SVTTPP-AP 177

QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHIFKQPFKTTGAQE 235
 DB 178 AREPGHSPQIISFFLALTSTALLFLPFLTLRFSVWKGKRLLYIFKQPFMRPVQTQOE 237

QY 236 EDACSCRCPOEEGG 250
 DB 238 EDGCSRFPPEEEGG 252

RESULT 26
 AA04174
 ID AA04174 standard; protein; 255 AA.
 AC AA04174;
 XX
 XX 12-DEC-1996 (first entry)
 DT
 DE Human receptor H4-1BB.
 XX
 KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
 KW B-lymphocyte; B-cell; immunostimulant; cancer; autoimmune disease;
 KW graft rejection; therapy.
 XX
 OS Homo sapiens.
 XX

PN WO9629348-A1.
 PD 26-SEP-1996.
 XX 22-MAR-1996; 96WO-US003965.
 XX 23-MAR-1995; 95US-00409851.
 XX (INDV) UNIV INDIANA FOUND.
 PA Kwon BS, Kang C;
 PI WPI; 1996-443138/44.
 DR N-PSDB; AAT39546.
 XX Monoclonal antibody specific for human receptor protein 4-1BB - used to enhance proliferation and activation of T-cells for treatment of cancer and to inhibit specific ligand binding for treating autoimmune diseases.
 PT Disclosure; Page 36-37; 48pp; English.
 XX Novel human receptor protein H4-1BB (AAW04174) has the potential to function as an accessory signaling molecule during T-cell activation and proliferation. Its amino acid sequence was deduced from a cDNA clone (AAT39546) isolated from activated human T-lymphocytes. Recombinant H4-1BB can be produced in transfected host cells. It is used to isolate receptor ligands, to stimulate B-cells expressing such ligands and to block H4-1BB ligand binding. A fusion protein of H4-1BB with human placental alkaline phosphatase can be used to modify immune responses. A monoclonal antibody raised against an immunopeptide (see also AAW04172) of H4-1BB is useful in the treatment of cancer and autoimmune diseases
 XX Sequence 255 AA;
 SQ

Query Match 54.8%; Score 782; DB 2; Length 255;
 Best Local Similarity 58.0%; Pred. No. 2.5e-56;
 Matches 148; Conservative 31; Mismatches 68; Indels 8; Gaps 6;

QY 1 MGNVCYNVIVLLVGGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSPSTFSSIGQP 59
 DB 1 MGNVCYNIVATLLVLPNFTSRSLQPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGQR 60
 QY 60 NCNCRVAGYFRFKPCSSSTHNAECIEGFCGLGQCTCEKDCRPGQELTKGCKTC 119
 DB 61 TCDICRQCKGVFRTRKESSTSNACEDCTPGFHLGAGCSMCEQDCRQGLTKGCKDC 120
 QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPBGGP 179
 DB 121 CFGTFNDQK-RGICRFPWTNCSLDGKSVLVNGTKERDVVCGSPADLSPGAS-SVTPP-AP 177
 QY 180 G---GHSLOVTLFLATLS-ALLIALFITLLFSLVKWIRKPPHIFKQPKKTTGAQE 235
 DB 178 AREPGHSQIISFFLATSTALLFLFLFSLVWVRGRKLLYIFKQPFMPVQTQ 237
 QY 236 EDACSCRCPEEEGG 250
 DB 238 EDGSCRCPEEEGG 252

RESULT 27
 ID AAR74087
 XX AAR74087 standard; protein; 255 AA.
 XX AAR74087;
 DT 21-JAN-1996 (first entry)
 DE Human receptor induced by lymphocyte activation (ILA).
 KW ILA; receptor inducible by lymphocyte activation; disease diagnosis;
 XX antiinflammatory.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..17
 FT /note= "signal peptide"
 FT Misc-difference 138
 FT /note= "potential N-glycosylation site"
 FT Misc-difference 149
 FT /note= "potential N-glycosylation site"
 FT Domain 187..213
 FT /note= "transmembrane domain"
 FT Misc-difference 234
 FT /note= "casein-kinase-II phosphorylation site"
 FT Misc-difference 235
 FT /note= "casein-kinase-II phosphorylation site"
 FT Binding-site 241..244
 FT /note= "potential ligand binding site"
 FT Misc-difference 242
 FT /note= "protein-kinase phosphorylation site"
 XX CA2108401-A.
 XX 28-MAR-1995.
 XX 14-OCT-1993; 93CA-02108401.
 XX 27-SEP-1993; 93US-00127693.
 XX (REGC) UNIV CALIFORNIA.
 XX Lotz M, Schwarz H;
 XX WPI; 1995-194420/26.
 XX N-PSDB; AAR74087.
 XX New receptor inducible by lymphocyte activation - used to develop prods. for the diagnosis and treatment of inflammatory host defence pathology.
 XX Claim 55; Page 61; 91pp; English.
 XX ILA may be used to identify a host defence inflammatory response in body tissue. The ILA agents can be used to detect an ILA-mediated pathology such as atherosclerosis, autoimmune disease (rheumatoid arthritis, CC transplant rejection, pathogenic host defense responses to microorganism and malignancy such as lung carcinoma
 XX Sequence 255 AA;
 SQ

Query Match 53.8%; Score 768; DB 2; Length 255;
 Best Local Similarity 57.6%; Pred. No. 3.5e-55;
 Matches 147; Conservative 30; Mismatches 70; Indels 8; Gaps 6;
 QY 1 MGNVCYNVIVLLVGGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSPSTFSSIGQP 59
 DB 1 MGNVCYNIVATLLVLPNFTSRSLQPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGQR 60
 QY 60 NCNCRVAGYFRFKPCSSSTHNAECIEGFCGLGQCTCEKDCRPGQELTKGCKTC 119
 DB 61 TCDICRQCKGVFRTRKESSTSNACEDCTPGFHLGAGCSMCEQDCRQGLTKGCKDC 120
 QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPBGGP 179
 DB 121 CFGTFNDQK-RGICRFPWTNCSLDGKSVLVNGTKERDVVCGSPADLSPGAS-SVTPP-AP 177
 QY 180 G---GHSLOVTLFLATLS-ALLIALFITLLFSLVKWIRKPPHIFKQPKKTTGAQE 235
 DB 178 AREPGHSQIISFFLATSTALLFLFLFSLVWVRGRKLLYIFKQPFMPVQTQ 237
 QY 236 EDACSCRCPEEEGG 250
 DB 238 EDGSCRCPEEEGG 252

Db	1	MGSCNYIVATLLLVNFERTSLQDPCSNCP-----	32
Qy	61	CNIRVCAGYFRKFKFCSSSTHNAECCEIEGPHCLGPOCTRCEKDCRQGOELTKQGCKTCS	120
Db	33	-----AGVFRTRKCSSTSNACDCITPGPHCLGAGCSNCEQCKQGOELTKKGCKDCC	95
Qy	121	LGFNFQNGTGVCRPWNTGSLDGRSVLTKTGTTEKDVVCGPVPVSFSSTTISVTPSGGPG	180
Db	86	FGTFNDQK-RGICRPWTNCSLGKSVLNGTKERDWWCGPSSADLSPGAS-SVTPP-AZA	142
Qy	181	---GHSLOVLTFLALTS-ALLALIFITLLFSLVKIRKFKPHIFKQPFKKTGAQEE	236
Db	143	REGHSPQIIISFLALTSTALLFLFLLTALFSLFVSVKGRKKLLYIFKQPFMRPVQTQEE	202
Qy	237	DACSCRCPOEEGG	250
Db	203	DGSCRFPEEEGG	216

RESULT 30	
AAW92524	
AAW92524	standard; protein; 219 AA.
XX	
AC	AAW92524;
XX	
DT	23-APR-1999 (first entry)
XX	
XX	Human h4-1BSV receptor protein variant.
DE	
XX	
XX	h4-1BSV receptor; human; splice variant; antagonist; treatment;
KW	disease prevention; endotoxic shock; inflammation; cerebral malaria;
KW	HIV virus activation; graft rejection; bone resorption; cachexia;
XX	gene therapy.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	Key
XX	Location/Qualifiers
FT	Misc-difference 33..34
FT	/note= "Site of deletion of residues GTFCNNRNRQICSPC
FT	PNFSFSSAGGRICDRCQCK corresponding to amino acid
FT	residues 34-69 of the wild-type protein"
XX	
XX	US5874240-A.
PN	

XX	US5874240-A.	
PN		
XX		
XX	23-FEB-1999.	
PD		
XX		
PF	13-MAR-1997;	97US-00815605.
XX		
XX		
PR	15-MAR-1996;	96US-0013474P.
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA		
XX		
PI	Dillon EJ, Yu G, Ni J, Gentz R;	
XX		
XX	WPI; 1999-179974/15.	
XX		
XX		
PT	New nucleic acid encoding human 4-LBB receptor splicing variant - useful	
PT	in treating H4-LBBSV mediated disease states such as endotoxic shock,	
PT	inflammation, graft rejection and inactivation of HIV.	
XX		
XX	Claim 29; Page; 28pp; English.	
PS		

Sequence 219 AA;

```

Query Match. 45.9%; Score 656; DB 2; Length 219;
Best Local Similarity 51.2%; Pred. No. 4.9e-46;
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;

Qy 1 MGNVNVVIVILLVGCCKVGVAVNSCDNCQPGTFCRKNPVCKSPSTFSSIGGQPN 60
Db 1 MGNVNVVIVILLVGCCKVGVAVNSCDNCQPGTFCRKNPVCKSPSTFSSIGGQPN 32
Qy 61 CNICRVAGYFRPKKFCSSSTHNAECIEGFHCLGPGQTRCEKDCRPGQELTKQGCKTCS 120
Db 33 -----AGVFRTRKBCSSSTHNAECDCTFGFHCLGAGCSMCEQDCQGGQELTKGCKDC 85
Qy 121 LGTFNDQNGTGVCRPWNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
Db 86 FGTFNDQK-RGICRPWNCSLDGRSVLVNGTKERDVVCGPSADUSFGAS-SVTPP-APA 142
Qy 181 ---GHSQVLTLFLAITS-ALLIALIFITLFSVLKWKRPKPHIFKQPKKTTGAAQEE 236
Db 143 REPCHSPQIISFPALTSTALLFLFLTRFSVXGRKLLYIFKQPFMRPVQTQEE 202
Qy 237 DACSCRCPOEEGG 250
Db 203 DGSCRFPEEEGG 216

RESULT 31
AAE08545
ID AAE08545 standard; protein; 219 AA.
AC AAE08545;
XX
XX
XX 15-NOV-2001 (first entry)
XX
XX Human h4-1BB splicing variant (h4-1BBSV) receptor.
XX
XX Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;
XX tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxic shock;
XX wound healing; autoimmune disease; acquired immunodeficiency syndrome;
XX AIDS; graft-host rejection; cellular proliferation; cerebral malaria;
XX bone resorption; human immunodeficiency virus; HIV; graft rejection;
XX inflammation; antibacterial; immunosuppressive; vulnery; vasotropic;
XX antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..18
XX FT FT /label= Signal_peptide
XX FT FT 19..219
XX FT FT /label= Mature_human_h4-1BBSV_receptor
XX FT FT 19..150
XX FT FT /label= Extracellular_domain
XX FT FT 151..177
XX FT FT /label= Transmembrane_domain
XX
XX US2001014465-A1.
XX
XX
XX 16-AUG-2001.
XX
XX 19-DEC-2000; 2000US-00739394.
XX
XX 15-MAR-1996; 96US-0013474P.
XX 13-MAR-1997; 97US-00816605.
XX 22-FEB-1999; 99US-00253549.
XX
XX (NLIJ/) NI J.
XX (YUG/) YU G.
XX (GENT/) GENTZ R.
XX (DILL/) DILLON P J.
XX
XX Ni J, Yu G, Gentz R, Dillon PJ;
XX

```

DR WPI; 2001-529104/58.
 DR N-PSDB; AAD15246.
 XX New human 4-1BB receptor splicing variant polypeptides and
 PT polynucleotides, useful for research, diagnosis, prevention and treatment
 PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
 PT syndrome and graft rejection.
 XX Claim 15; Fig 1; 28pp; English.
 XX The present invention relates to an isolated human 4-1BB receptor
 CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
 CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
 CC gene therapy, h4-1BBSV is useful for research, biological, clinical and
 CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives
 CC are useful as an immunogen to produce antibodies which are useful for
 CC isolating and identifying clones expressing the polypeptide or to purify
 CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of
 CC disorders of cells, tissues and organisms and its nucleic acid is useful
 CC for detecting complementary polynucleotides for e.g. as a diagnostic
 CC reagent and for chromosomal identification. h4-1BBSV receptor agonists
 CC are useful for preventing, treating tumours, restenosis, cytotoxicity,
 CC bacterial and viral infection, deleterious effects of ionising radiation,
 CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-
 CC host rejection, to regulate immune responses, wound healing and cellular
 CC proliferation and antagonists are useful for treating and/or preventing
 CC endotoxic shock, inflammation, cerebral malaria, activation of human
 CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
 CC cachexia. The present sequence is human h4-1BBSV receptor
 XX
 SQ Sequence 219 AA;
 Query Match 45.9%; Score 656; DB 4; Length 219;
 Best Local Similarity 51.2%; Pred. No. 4.9e-46;
 Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;
 QY 1 MGNVCNIVVILLVCEKVGAVQNSCDNCPGTFCKRKNPVCKSPSTSSIGQPN 60
 DB 1 MGNVCNIVATLLVLFNFTSLQDPCSNCP----- 32
 QY 61 CNICRVACGVFRKFKCSSTHNAECIEGFHCLGPOCTRCXDCRPGQELTKQGCKTCS 120
 DB 33 -----AGVFRTRKCSSTHNAECIEGFHCLGACSCNCEQDKQGLTKQGCKDC 85
 QY 121 LGTFNDQNGTGVCRPWNKSLDGRSVLKTGTTKDVVCGPPVVSFSTTISVTPGGPG 180
 DB 86 FGTFDQK-RGICRPWNKSLDGRSVLKTGTTKDVVCGPPVVSFSTTISVTPGGPG 142
 QY 181 ---CHSLOVLTFLATLS-ALLLALIFITLLFSLVKWIRKFKPHKPKKTTGAAQEE 236
 DB 143 REPGHSQIISFFALTSTALLFLFLFTLRFVSVVRGRKKLLYIFQPMRPVQTQEE 202
 QY 237 DACSCRCFQEEGG 250
 DB 203 DGCSCRPPEEEGG 216
 RESULT 32
 ABB84639
 ID ABB84639 standard; protein; 219 AA.
 XX
 AC ABB84639;
 XX
 XX 05-FEB-2003 (first entry)
 XX
 XX Human h4-1BBSV receptor.
 XX Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;
 KW anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator;
 KW vasotropic; gene therapy; chromosome mapping; extracellular domain;
 KW endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease;
 KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;
 KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;

KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;
 KW autoimmune disease.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..18
 FT Protein 19..219
 FT /label= leader_sequence
 FT /label= h4-1BBSV receptor
 FT /note= "region specifically claimed in claim 1b"
 FT Domain 19..150
 FT /label= soluble_extracellular_domain
 FT /note= "region specifically claimed in claim 1a"
 FT Domain 151..177
 FT /label= transmembrane_domain
 XX US2002127651-A1.
 PN 12-SEP-2002.
 XX 15-MAR-2002; 2002US-00097330.
 XX 15-MAR-1996; 96US-0013474P.
 PR 13-MAR-1997; 97US-00816605.
 PR 22-FEB-1999; 99US-00253549.
 PR 19-DEC-2000; 2000US-00739394.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ni J, Yu G, Gentz RL, Dillon PJ;
 PI WPI; 2003-066900/06.
 DR N-PSDB; ABS57520.
 XX Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,
 PT providing resistance to bacteria, viruses and parasites, to induce
 PT proliferation of endothelial cells, and to treat restenosis.
 PS Example 2; Fig 1A-B; 29pp; English.
 XX This invention describes a novel human h4-1BBSV receptor or a sequence
 CC that is at least 85% identical to the h4-1BBSV receptor. The product of
 CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,
 CC antibacterial, antiinflammatory, protozoacide, immunomodulator and
 CC vasotropic activity and can be used for gene therapy and chromosome
 CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to
 CC a disease related to underexpression of h4-1BBSV or for identifying
 CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV
 CC receptor polypeptide is useful for treating and/or preventing endotoxic
 CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human
 CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or
 CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired
 CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,
 CC viruses and parasites, to induce proliferation of endothelial cells and
 CC certain haematopoietic cells, to treat restenosis and to prevent certain
 CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.
 CC This sequence represents the human 4-1BBSV receptor described in the
 CC disclosure of the invention
 XX
 SQ Sequence 219 AA;
 Query Match 45.9%; Score 656; DB 6; Length 219;
 Best Local Similarity 51.2%; Pred. No. 4.9e-46;
 Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;
 QY 1 MGNVCNIVVILLVCEKVGAVQNSCDNCPGTFCKRKNPVCKSPSTSSIGQPN 60
 DB 1 MGNVCNIVATLLVLFNFTSLQDPCSNCP----- 32
 QY 61 CNICRVACGVFRKFKCSSTHNAECIEGFHCLGPOCTRCXDCRPGQELTKQGCKTCS 120
 DB 33 -----AGVFRTRKCSSTHNAECIEGFHCLGACSCNCEQDKQGLTKQGCKDC 85

CC The present invention describes peptides and peptide analogues which
 CC correspond in primary sequence to a binding loop of a tumour necrosis
 CC factor receptor (TNF-R) superfamily member. The compounds are especially
 CC designed from a binding loop of TNF-R p55. They are capable of inhibiting
 CC TNF binding to its cellular receptors and may be used to inhibit the
 CC biological activities of TNF. They may be used in treating TNF-associated
 CC conditions such as acute and chronic inflammatory responses, septic
 CC shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic
 CC reactions, immune complex disease, transplantation rejection and malaria.
 CC Administration is, e.g. oral, transdermal, transmucosal, pulmonary,
 CC subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5
 CC mg/kg/day. The present sequence represents an extracellular Cys-rich
 CC domain of TNF-R from the present invention
 XX
 SQ Sequence 69 AA;
 Query Match 18.8%; Score 268; DB 2; Length 69;
 Best Local Similarity 63.8%; Pred. No. 1.2e-14;
 Matches 44; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
 QY 44 CKSPPTFSIGQPNICRYCAGYFRFKFCSSTHNAECIEGPHCLGPOCTRCEK 103
 DB 1 CSPCPNPSFSSAGGQRTCDICRCKGVFRTRKCSSTNAECDCTPGFHLGAGCSMCQ 60
 QY 104 DCRPGQELT 112
 DB 61 DCKQGOELT 69
 RESULT 35
 AAB69202
 ID AAB69202 standard; protein; 69 AA.
 XX
 AC AAB69202;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Human TNF-R extracellular Cys-rich domain 4-IBB SEQ ID NO:11.
 XX
 KW Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
 KW osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic;
 KW antirheumatic; antiarthritic; antiinflammatory; immunomodulatory;
 KW tumour necrosis factor-related activation-induced cytokine; TRANCE;
 KW receptor activator of NF-kappaB ligand; RANK; osteoporosis;
 KW Paget's disease; metastatic bone disease; rheumatoid arthritis;
 KW periodontal disease; modulating dendritic cell maturation;
 KW T cell proliferation; CD40 receptor system.
 XX
 OS Homo sapiens.
 XX
 PN WO200108699-A1.
 XX
 PD 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-US020510.
 XX
 PR 28-JUL-1999; 99US-0146090P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 PA (AOKI/) AOKI K.
 PA (HORN/) HORNE W C.
 PA (BARO/) BARON R.
 XX
 PI Aoki K, Horne WC, Baron R, Greene MI, Murali R;
 XX
 DR WPI; 2001-182866/18.
 XX
 PT Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for
 PT inhibiting osteoclastogenesis and bone resorption.
 XX
 PS Disclosure; Fig 1; 81pp; English.
 XX
 CC The present invention describes a method for inhibiting

CC osteoclastogenesis and bone resorption. Osteoclastogenesis and bone
 CC resorption inhibiting peptide analogues from the present invention have
 CC osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory
 CC and immunomodulatory activities, and are tumour necrosis factor (TNF)-
 CC related activation-induced cytokine (TRANCE)/receptor activator of NF-
 CC kappaB ligand (RANK) inhibitors. The method is useful for treating
 CC diseases characterized by bone loss such as osteoporosis, Paget's
 CC disease, metastatic bone disease, rheumatoid arthritis or periodontal
 CC disease, and modulating dendritic cell maturation, T cell proliferation,
 CC and/or CD40 receptor systems. The present sequence represents an
 CC extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-
 CC R) superfamily member, which is used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 69 AA;
 Query Match 18.8%; Score 268; DB 4; Length 69;
 Best Local Similarity 63.8%; Pred. No. 1.2e-14;
 Matches 44; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
 QY 44 CKSPPTFSIGQPNICRYCAGYFRFKFCSSTHNAECIEGPHCLGPOCTRCEK 103
 DB 1 CSPCPNPSFSSAGGQRTCDICRCKGVFRTRKCSSTNAECDCTPGFHLGAGCSMCQ 60
 QY 104 DCRPGQELT 112
 DB 61 DCKQGOELT 69
 RESULT 36
 AAB36700
 ID AAB36700 standard; protein; 415 AA.
 XX
 AC AAB36700;
 XX
 DT 15-MAR-2001 (first entry)
 XX
 DE Human tumour necrosis factor receptor LTBR protein SEQ ID NO:6.
 XX
 KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neurotropic;
 KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
 KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
 KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
 KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
 KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
 KW apoptotic cell death related disease; autoimmune disorder;
 KW cardiovascular disorder; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN WO2000071150-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 18-MAY-2000; 2000WO-US013515.
 XX
 PR 20-MAY-1999; 99US-0135164P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Wei Y, Ruben SM, Gentz RL, Ni J;
 XX
 DR WPI; 2001-041051/05.
 XX
 PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or
 PT prevention of cancer, autoimmune disorders and viral infection.
 XX
 PS Disclosure; Fig 2; 285pp; English.
 XX
 CC The present invention describes the human TRID protein (tumour necrosis
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
 CC intracellular domain, also referred to as tumour necrosis factor receptor

CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, neurotropic,
 CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
 CC activities, and can be used in gene therapy. The TRID polynucleotides are
 CC useful for detecting complementary polynucleotides. TRID proteins and
 CC polynucleotides are useful in the treatment of tumours, resistance to
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.
 CC They are also useful for inducing proliferation of T-cells, endothelial
 CC cells and certain haematopoietic cells, to regulate antiviral responses
 CC and to prevent certain autoimmune diseases after stimulation of TRID by
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
 CC polypeptides are useful for treating and/or preventing diseases
 CC associated with increased or decreased apoptotic cell death. The TRID
 CC polynucleotides, proteins, antibodies, agonists and antagonists are
 CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)
 CC autoimmune disorders; (c) diseases associated with increased apoptosis;
 CC (d) cardiovascular disorders; and (e) viral infection. The present
 CC sequence represents a tumour necrosis factor receptor used in comparison
 CC with TRID in the exemplification of the present invention

XX SQ Sequence 415 AA;

Query Match 16.6%; Score 237; DB 4; Length 415;
 Best Local Similarity 27.0%; Pred. No. 3e-11;
 Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCPGTF-----CRKNPVCKSCPPSTFSSIGGQ-PNCNICRVACGYFRFKX--CSS 79
 Db 59 CSRCPGGEFVAVCSRSQDTVCKTCHNSYNHNLSTCQLCRPCDVLGFEEVAPCTS 118
 QY 80 THNAECECEGPHC--LGPQCTRCEDK---CRGQEL-----TKQGKTCSLGTF- 124
 Db 119 DRKACRCQPGMSCVYLNDNECHVEERLVCQPGTEAEVTDINDTVNCPCKPGHFQ 178
 QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVVSFSPSTTISVTPEGGPGGHS 184
 Db 179 NTSSPRACQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
 QY 185 QVLTFLALTALLLALIFITLLFSLVKWIR-----KKFPHFKOPFKKTTGAAQEDAC 239
 Db 269 PCPAPRAD 276

RESULT 37
 ID ABP96138
 AC ABP96138;
 XX
 DI 09-MAY-2003 (first entry)

DE Mouse lymphotoxin-beta receptor protein SEQ ID NO:20.

KW Human; tumour necrosis factor receptor 2 related protein variant;
 KW TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
 KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
 KW asthma; ulcerative colitis.

XX Mus musculus.

XX WO2003012037-A2.

PD 13-FEB-2003.

XX 24-JUL-2002; 2002WO-US023684.

XX 27-JUL-2001; 2001US-00917372.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal PG, Warren BA;
 XX WPI; 2003-256445/25.

XX New cDNA, useful for preparing a composition for treating a disease or
 PT condition associated with increased TNF signaling e.g., cancer of the
 PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
 PT rheumatoid arthritis, asthma.

XX Disclosure; Fig 2A-C; 64pp; English.

XX The present invention describes human tumour necrosis factor receptor 2
 CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic
 CC and immunosuppressive activities, and can be used in gene therapy. The
 CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
 CC for treating a disease or condition associated with increased TNF
 CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
 CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
 CC arthritis, asthma or ulcerative colitis. The present sequence represents
 CC a mouse lymphotoxin-beta receptor amino acid sequence, which is given in
 CC comparison with human TNFR2PV in the exemplification of the present
 CC invention

XX SQ Sequence 415 AA;

Query Match 16.6%; Score 237; DB 6; Length 415;
 Best Local Similarity 27.0%; Pred. No. 3e-11;
 Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCPGTF-----CRKNPVCKSCPPSTFSSIGGQ-PNCNICRVACGYFRFKX--CSS 79
 Db 59 CSRCPGGEFVAVCSRSQDTVCKTCHNSYNHNLSTCQLCRPCDVLGFEEVAPCTS 118
 QY 80 THNAECECEGPHC--LGPQCTRCEDK---CRGQEL-----TKQGKTCSLGTF- 124
 Db 119 DRKACRCQPGMSCVYLNDNECHVEERLVCQPGTEAEVTDINDTVNCPCKPGHFQ 178
 QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVVSFSPSTTISVTPEGGPGGHS 184
 Db 179 NTSSPRACQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
 QY 185 QVLTFLALTALLLALIFITLLFSLVKWIR-----KKFPHFKOPFKKTTGAAQEDAC 239
 Db 220 --AMLLALLSLVLFLLFTTVL--ACAWMRHPSLCRKLGLTKR-----HPEGES 268
 QY 240 SCRCPOEE 247
 Db 269 PCPAPRAD 276

RESULT 38
 AAW83200
 ID AAW83200 standard; protein; 625 AA.
 XX
 AC AAW83200;
 XX
 DT 11-FEB-1999 (first entry)

DE Murine osteoclast differentiation and activation receptor.

XX Osteoprotegerin binding protein; OPG binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease.

XX Mus sp.

XX WO9846751-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-US007584.

XX PR 16-APR-1997; 97US-00842842.
XX PR 23-JUN-1997; 97US-00880855.
XX PR 30-MAR-1998; 98US-00052521.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ;
XX DR WPI; 1998-594578/50.
XX DR N-PSDB; AAV70304.
XX PT Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g.
XX PT treating bone diseases by modulating osteoclast differentiation and for
XX PT diagnosis.
XX PS Example 12; Fig 10; 47pp; English.
XX PS The present sequence represents murine osteoclast differentiation and
CC activation receptor (ODAR). The present invention describes
CC osteoprotegrin (OPG) binding protein. Host cells transfected with
CC vectors containing nucleic acid molecules encoding OPG binding protein
CC are used to produce recombinant OPG binding protein. OPG binding protein
CC is used in binding assays to determine osteoprotegrin (OG) in biological
CC samples; to screen for specific binding agents (particularly agonists and
CC antagonists, including intracellular proteins); to raise Ab (useful in
CC immunoassays for detection of OPG binding protein) and to identify
CC compounds that modulate binding of OPG binding protein to ODAR. The
CC nucleic acid molecule encoding OPG binding protein can be used to detect
CC OPG binding protein-encoding sequences, e.g. screening for related
CC sequences, also to produce transgenic animal models, while complementary
CC expression. Modulators of OPG binding protein, particularly soluble forms
CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,
CC e.g. osteoporosis, bone loss caused by arthritis or metastases,
CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,
CC loosening of prostheses, optionally in combination with agents that
CC promote bone growth
XX SQ Sequence 625 AA;
Query Match 15.1%; Score 215; DB 2; Length 625;
Best Local Similarity 28.6%; Pred. No. 3e-09;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;
QY 28 CDNCQPGTF-CRKNP-----VKSCPPSTF-SSIGQPNICNCRVCAGYFRFKFCSSTH 81
DB 48 CSRCEPKYLSKCTPTSDSVCLPCGDEYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECCIEGFH----CLGPQCTCEKDCRPG-----QELTKQG-CKTCSLGTNDQ- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLNKNKDTVCTPCLLGFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGHSLQV 186
DB 165 SSTDKCKPWNCTLLGKLEAHQGTTESDVVC-----SSMTLRPPKRAQAYLPSLIV 217
QY 187 LTFLALTSALLALIF-----ITLFSVLKWKIRKFPFHFKQPKKTTGAQEEDA 238
DB 218 LLLFISV--VVVAALFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCECPQEEGG 250
DB 255 CSSLSGNKSSG 266
RESULT 39
AAW69958
ID AAW69958 standard; protein; 625 AA.
XX AC AAW69958;
XX DT 08-OCT-1998 (first entry)

XX DE Murine NF-kB receptor activator muRANK.
XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX KW immune response; inflammatory response; toxic shock; sepsis; RANKL;
XX KW RANK ligand; tumour necrosis factor; TNF; murine.
XX OS Mus sp.
XX XX WO9828426-A2.
XX PN 02-JUL-1998.
XX PD 22-DEC-1997; 97WO-US023775.
XX PF 23-DEC-1996; 96US-0059978P.
XX PR 07-MAR-1997; 97US-00813509.
XX PR 14-OCT-1997; 97US-0064671P.
XX XX (IMMV) IMMUNEX CORP.
XX PA Anderson DM, Galibert LJ, Maraskovsky E;
XX PI WPI; 1998-377657/32.
XX DR N-PSDB; AAV41379.
XX DR New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells.
XX PS Example 14; Page 62-64; 80pp; English.
XX PS This represents the murine muRANK (receptor activator of necrosis factor-
CC kappaB (NF-kB)) polypeptide which is a homolog of the human RANK. RANK is
CC a member of the tumour necrosis factor (TNF) family. A soluble RANK may
CC be used for inhibiting activation of NF-kB by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used
CC to induce maturation of dendritic cells and enhance their allo-
CC stimulatory capacity, thereby augmenting an immune response. The soluble
CC RANK polypeptide composition may also be used for regulating an immune or
CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be
CC useful in ameliorating negative effects of an inflammatory response that
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
CC graft-versus-host reactions, or acute inflammatory reactions. They can
CC also be used in adjunct therapy for disease characterised by neoplastic
CC cells that express RANK. RANKL polypeptides can also be used to identify
CC inhibitors of RANK and thus inhibitors of an inflammatory response, and
CC also for protecting RANK-expressing cells from the negative effects of
CC chemotherapy or the presence of high levels of TNF-alpha. The products
CC can also be used for detection and drug screening
XX SQ Sequence 625 AA;
Query Match 15.1%; Score 215; DB 2; Length 625;
Best Local Similarity 28.6%; Pred. No. 3e-09;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;
QY 28 CDNCQPGTF-CRKNP-----VKSCPPSTF-SSIGQPNICNCRVCAGYFRFKFCSSTH 81
DB 48 CSRCEPKYLSKCTPTSDSVCLPCGDEYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECCIEGFH----CLGPQCTCEKDCRPG-----QELTKQG-CKTCSLGTNDQ- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLNKNKDTVCTPCLLGFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGHSLQV 186
DB 165 SSTDKCKPWNCTLLGKLEAHQGTTESDVVC-----SSMTLRPPKRAQAYLPSLIV 217
QY 187 LTFLALTSALLALIF-----ITLFSVLKWKIRKFPFHFKQPKKTTGAQEEDA 238
DB 218 LLLFISV--VVVAALFGVYRKGGKALTANLWNV-----NDA 254

QY 239 CSCRCPOBEEGG 250
 Db 255 CSSLSGNKESG 266

RESULT 40
 AAW68294
 ID AAW68294 standard; protein; 625 AA.
 AC AAW68294;
 XX 08-OCT-1998 (first entry)
 DT Murine NF-kB receptor activator muRANK.
 DE
 XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis; RANKL;
 KW RANK ligand; tumour necrosis factor; TNF; murine.
 XX
 OS Mus sp.
 XX
 FN WO9828424-A2.
 XX
 XX 02-JUL-1998.
 XX 22-DEC-1997; 97WO-US023866.
 XX 23-DEC-1996; 96US-0059978P.
 PR 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 XX
 DR WPI; 1998-377655/32.
 DR N-PSDB; AAV41373.
 XX
 PT New isolated receptor activator of necrosis factor-kappa B - useful for,
 PT e.g. developing products for regulating an immune or inflammatory
 PT response, treating toxic shock or sepsis.
 XX
 PS Claim 27; Page 62-64; 80pp; English.
 XX
 CC This represents the murine muRANK (receptor activator of necrosis factor-
 CC kappaB (NF-kB)) polypeptide which is a homolog of the human RANK. RANK is
 CC a member of the tumour necrosis factor (TNF) family. Host cells
 CC transformed or transfected with an expression vector comprising the RANK
 CC encoding nucleic acid can be used to produce recombinant RANK protein.
 CC The soluble RANK may be used for inhibiting activation of NF-kB, by
 CC contacting a cell expressing membrane-associated RANK with a soluble RANK
 CC which binds to RANK ligand (RANKL). The soluble RANK polypeptide
 CC composition may also be used for regulating an immune or inflammatory
 CC response. Inhibition of NF-kB by RANK antagonists may be useful in
 CC ameliorating negative effects of an inflammatory response that result
 CC from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-
 CC versus-host reactions, or acute inflammatory reactions. They can also be
 CC used in adjunct therapy for disease characterised by neoplastic cells
 CC that express RANK. The products can also be used for detection and drug
 CC screening
 XX
 SQ Sequence 625 AA;

Search completed: May 5, 2004, 14:38:04
 Job time : 129.123 secs

Query Match 15.1%; Score 215; DB 2; Length 625;
 Best Local Similarity 28.6%; Pred. No. 3e-09;
 Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----YKSCPPSTF-SSIGGPNICRVCAGYFRFKFCSSTH 81
 Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGGDEYLDTWNEEDKLLHKVCDAGKALVADPGNH 107
 QY 82 NA--ECBCIEGFH-----CLGQCTRCBCKCRPG-----QELTKQG-CKTCSLGTNDQ- 127

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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:35:32 ; Search time 36.8219 Seconds
(without alignments)
358.923 Million cell updates/sec

Title: US-10-067-122b-2
Perfect score: 1428
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCUTS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1428	100.0	256	1	US-08-236-918A-6 Sequence 6, Appl
2	1428	100.0	256	4	US-09-150-864A-6 Sequence 6, Appl
3	1428	100.0	256	4	US-08-012-269A-2 Sequence 2, Appl
4	1428	100.0	256	4	US-09-623-545A-3 Sequence 3, Appl
5	1428	100.0	256	5	PCT-US86-03965-2 Sequence 2, Appl
6	1085	76.0	191	3	US-08-974-022-52 Sequence 52, Appl
7	1085	76.0	191	3	US-08-795-445A-52 Sequence 52, Appl
8	1085	76.0	191	3	US-08-795-447A-52 Sequence 52, Appl
9	1085	76.0	191	3	US-08-974-186-52 Sequence 52, Appl
10	1085	76.0	191	3	US-08-795-446B-52 Sequence 52, Appl
11	1085	76.0	191	4	US-08-706-945D-139 Sequence 139, App
12	1085	76.0	191	4	US-08-577-788C-53 Sequence 53, App
13	795	55.7	255	1	US-08-236-918A-8 Sequence 8, Appl
14	795	55.7	255	2	US-08-816-605-9 Sequence 9, Appl
15	795	55.7	255	3	US-09-006-353A-11 Sequence 11, Appl
16	795	55.7	255	4	US-09-007-097-2 Sequence 2, Appl
17	795	55.7	255	4	US-09-150-864A-8 Sequence 8, Appl
18	795	55.7	255	4	US-09-573-986-11 Sequence 11, Appl
19	795	55.7	255	4	US-09-578-764A-2 Sequence 2, Appl
20	795	55.7	255	4	US-09-623-545A-2 Sequence 2, Appl
21	795	55.7	255	5	PCT-US86-03965-8 Sequence 8, Appl
22	656	45.9	219	2	US-08-816-605-2 Sequence 55, Appl
23	497	34.8	132	4	US-09-523-323-55 Sequence 2, Appl
24	268	18.8	69	3	US-08-866-545-11 Sequence 11, Appl
25	268	18.8	69	4	US-09-627-775-11 Sequence 11, Appl
26	237	16.6	415	3	US-09-006-353A-6 Sequence 6, Appl
27	237	16.6	415	4	US-09-573-986-6 Sequence 6, Appl

28 215 15.1 625 3 US-08-996-139-15 Sequence 15, Appl
29 215 15.1 625 3 US-08-995-659-15 Sequence 15, Appl
30 215 15.1 625 3 US-09-215-649A-15 Sequence 15, Appl
31 215 15.1 625 4 US-09-577-780-15 Sequence 15, Appl
32 215 15.1 625 4 US-09-577-800-15 Sequence 15, Appl
33 215 15.1 625 4 US-09-466-496-15 Sequence 15, Appl
34 215 15.1 625 4 US-09-871-856-15 Sequence 15, Appl
35 215 15.1 625 4 US-09-871-291-15 Sequence 15, Appl
36 215 15.1 625 4 US-09-877-650-15 Sequence 27, Appl
37 208.5 14.6 276 3 US-09-041-886-27 Sequence 10, Appl
38 208.5 14.6 277 3 US-09-042-785A-10 Sequence 10, Appl
39 208.5 14.6 277 3 US-09-006-353A-10 Sequence 2, Appl
40 208.5 14.6 277 4 US-08-114-344D-2 Sequence 10, Appl
41 208.5 14.6 277 4 US-09-573-986-10 Sequence 2, Appl
42 208.5 14.6 277 4 US-08-338-975A-2 Sequence 6, Appl
43 205.5 14.4 240 4 US-09-512-363-6 Sequence 6, Appl
44 205.5 14.4 240 4 US-09-176-200-6 Sequence 4, Appl
45 205.5 14.4 451 3 US-08-996-139-4

ALIGNMENTS

RESULT 1
US-08-236-918A-6
; Sequence 6, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-6

Query Match 100.0%; Score 1428; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGNNCYVNVVILLVGCEKVGAVQNCDCQPGTFCRKNPVCKSCPPSTFSSIGQPN 60

Db 1 MGNCCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVACAGYFRFKFCSSTHNAECIEGFGHCLGPOCTRCCKRCPGQELTKQCKTCS 120
Db 61 CNICRVACAGYFRFKFCSSTHNAECIEGFGHCLGPOCTRCCKRCPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTVCVRPWTNCSLDGRSVLTKGTTEKDVVCGPPVWVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTVCVRPWTNCSLDGRSVLTKGTTEKDVVCGPPVWVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKOPPKKTTGAAQEDACS 240
Db 181 GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKOPPKKTTGAAQEDACS 240
QY 241 CRCPOEEGGGGYEL 256
Db 241 CRCPOEEGGGGYEL 256

RESULT 2

US-09-150-864A-6
; Sequence 6, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150.864A
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus sp. (clone: mu4-1BB)
US-09-150-864A-6

Query Match 100.0%; Score 1428; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-116;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNCCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNCCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVACAGYFRFKFCSSTHNAECIEGFGHCLGPOCTRCCKRCPGQELTKQCKTCS 120
Db 61 CNICRVACAGYFRFKFCSSTHNAECIEGFGHCLGPOCTRCCKRCPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTVCVRPWTNCSLDGRSVLTKGTTEKDVVCGPPVWVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTVCVRPWTNCSLDGRSVLTKGTTEKDVVCGPPVWVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKOPPKKTTGAAQEDACS 240
Db 181 GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKOPPKKTTGAAQEDACS 240
QY 241 CRCPOEEGGGGYEL 256
Db 241 CRCPOEEGGGGYEL 256

RESULT 3

US-08-012-269A-2
; Sequence 2, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:

; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-012-269A-2

Query Match 100.0%; Score 1428; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNCCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNCCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVACAGYFRFKFCSSTHNAECIEGFGHCLGPOCTRCCKRCPGQELTKQCKTCS 120
Db 61 CNICRVACAGYFRFKFCSSTHNAECIEGFGHCLGPOCTRCCKRCPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTVCVRPWTNCSLDGRSVLTKGTTEKDVVCGPPVWVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTVCVRPWTNCSLDGRSVLTKGTTEKDVVCGPPVWVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKOPPKKTTGAAQEDACS 240
Db 181 GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKOPPKKTTGAAQEDACS 240
QY 241 CRCPOEEGGGGYEL 256
Db 241 CRCPOEEGGGGYEL 256

RESULT 4

US-09-623-545A-3
; Sequence 3, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; FILE REFERENCE: 30424.1USWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-623-545A-3

Query Match 100.0%; Score 1428; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNCCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNCCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKYNPVCKSCPPSTFSSIGGQPN 60

QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGPHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
DB 61 CNICRVAGYFRFKFCSSSTHNAECIEGPHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
QY 181 GHSLOVLTFLALTSALLALIFITLLFSVLKWKIRKFPFHFKQPFKKTGAQBEDACS 240
DB 181 GHSLOVLTFLALTSALLALIFITLLFSVLKWKIRKFPFHFKQPFKKTGAQBEDACS 240
QY 241 CRCPQEEEGGGGYEL 256
DB 241 CRCPQEEEGGGGYEL 256

RESULT 5
PCT-US96-03965-2
; Sequence 2, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-Yuil
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03965
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KWO5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-03965-2

Query Match 100.0%; Score 1428; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVWVLLVGCCKYGVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60
DB 1 MGNNCYNVWVLLVGCCKYGVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60
QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGPHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
DB 61 CNICRVAGYFRFKFCSSSTHNAECIEGPHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGGPG 180
QY 181 GHSLOVLTFLALTSALLALIFITLLFSVLKWKIRKFPFHFKQPFKKTGAQBEDACS 240
DB 181 GHSLOVLTFLALTSALLALIFITLLFSVLKWKIRKFPFHFKQPFKKTGAQBEDACS 240
QY 241 CRCPQEEEGGGGYEL 256
DB 241 CRCPQEEEGGGGYEL 256

RESULT 6
US-08-974-022-52
; Sequence 52, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-52

Query Match 76.0%; Score 1085; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVWVLLVGCCKYGVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60
DB 1 MGNNCYNVWVLLVGCCKYGVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60
QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGPHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120

Db 61 CNICRVACGYFRFKFCSTHNAECIEGPHCLGPQCTRCCKDCRPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTGYCRPWTNCSLDGRSVLKTGTTGTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGYCRPWTNCSLDGRSVLKTGTTGTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTLFL 191
Db 181 GHSLOVLTLFL 191

RESULT 7
US-08-795-445A-52
; Sequence 52, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-52

Query Match 76.0%; Score 1085; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNNCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKYNPVCKSCPSTFSSIGGQPN 60
Db 1 MGNNCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKYNPVCKSCPSTFSSIGGQPN 60
QY 61 CNICRVACGYFRFKFCSTHNAECIEGPHCLGPQCTRCCKDCRPGQELTKQCKTCS 120
Db 61 CNICRVACGYFRFKFCSTHNAECIEGPHCLGPQCTRCCKDCRPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTGYCRPWTNCSLDGRSVLKTGTTGTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGYCRPWTNCSLDGRSVLKTGTTGTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTLFL 191
Db 181 GHSLOVLTLFL 191

RESULT 8
US-08-795-447A-52
; Sequence 52, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-447A-52

Query Match 76.0%; Score 1085; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNNCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKYNPVCKSCPSTFSSIGGQPN 60
Db 1 MGNNCYNVWVILLVGCCKVAVQNSCDNCPQGTFCRKYNPVCKSCPSTFSSIGGQPN 60
QY 61 CNICRVACGYFRFKFCSTHNAECIEGPHCLGPQCTRCCKDCRPGQELTKQCKTCS 120
Db 61 CNICRVACGYFRFKFCSTHNAECIEGPHCLGPQCTRCCKDCRPGQELTKQCKTCS 120
QY 121 LGTFNDQNGTGYCRPWTNCSLDGRSVLKTGTTGTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGYCRPWTNCSLDGRSVLKTGTTGTEKDVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTLFL 191
Db 181 GHSLOVLTLFL 191

RESULT 9
US-08-974-186-52
; Sequence 52, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:


```
;
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-52

Query Match 76.0%; Score 1085; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVGAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
Db 61 CNICRVGAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFL 191
Db 181 GHSLOVLTFL 191

RESULT 11
US-08-706-945D-139
; Sequence 139, Application US/08/706,945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-706-945D-139

Query Match 76.0%; Score 1085; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVGAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
Db 61 CNICRVGAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFL 191
Db 181 GHSLOVLTFL 191

RESULT 10
US-08-795-446B-52
; Sequence 52, Application US/08/795,446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-52

Query Match 76.0%; Score 1085; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVGAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
Db 61 CNICRVGAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFL 191
Db 181 GHSLOVLTFL 191
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Db 61 CNICRVAGYFRFKFCSTHNAECIEGPHCLGPOCTRCCKDRPQQLTKQGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFL 191
Db 181 GHSLOVLTFL 191

RESULT 12
US-08-577-788C-53
; Sequence 53, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-577-788C-53

Query Match 76.0%; Score 1085; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGNVCYNVWVILLVGCCKVAVQNSCDNCQPGTFCRKNPVCKSCPPSTFSSIGQPN 60
Db 1 MGNVCYNVWVILLVGCCKVAVQNSCDNCQPGTFCRKNPVCKSCPPSTFSSIGQPN 60
QY 61 CNICRVAGYFRFKFCSTHNAECIEGPHCLGPOCTRCCKDRPQQLTKQGCKTCS 120
Db 61 CNICRVAGYFRFKFCSTHNAECIEGPHCLGPOCTRCCKDRPQQLTKQGCKTCS 120
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY 181 GHSLOVLTFL 191
Db 181 GHSLOVLTFL 191

RESULT 13
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-236-918A-8
Query Match 55.7%; Score 795; DB 1; Length 255;
Best Local Similarity 58.4%; Pred. No. 9.1e-63;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNVCYNVWVILLVGCCKVAVQNSCDNCQPGTFCRKNPVCKSCPPSTFSSIGQPN 59
Db 1 MGNVCYNVWVILLVGCCKVAVQNSCDNCQPGTFCRKNPVCKSCPPSTFSSIGQPN 59
QY 60 CNICRVAGYFRFKFCSTHNAECIEGPHCLGPOCTRCCKDRPQQLTKQGCKTCS 119
Db 61 TCDICRQCKGVFRTRKESSTSNABCDCTPGHCLGAGCSMCEQDCKQQLTKKGCKDC 120
QY 120 SGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFTENDQK-RGICRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 177
QY 180 G---GHSLOVLTFLALTS-ALLALIFITLLFSLVKWIRKFFPHFKQPFKTTGAAQE 235
Db 178 AREPGHSFQIISFFLALTSTALLFLLFLLTULFVSVKGRKKLLYIFKQPFMRPVQTQEE 237
QY 236 EDACSCRCPOEEGG 250
Db 238 EDGCSRCFPEEEGG 252

RESULT 14
US-08-816-605-9
; Sequence 9, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-006-353A-11

Query Match 55.7%; Score 795; DB 3; Length 255;
Best Local Similarity 58.4%; Pred. No. 9.1e-63;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 59
DB 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 60
QY 60 NCNCRVACGYFRPKKFCSSSTHNAECIEGPHCLGPQCTRCEDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSMCEQDCKGQELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTP-AP 177
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHFKQPKFKTTGAAQE 235
DB 178 AREPGHSPQIISFFLALTSTALLFLFLLTRFSVVKRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACRCRCPQEEGG 250
DB 238 EDGCSRFPPEEEGG 252

RESULT 16
US-09-007-097-2
Sequence 2, Application US/09007097A
Patent No. 6303121
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung
TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
FILE REFERENCE: 740.011US1
CURRENT APPLICATION NUMBER: US/09/007,097A
CURRENT FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-007-097-2

Query Match 55.7%; Score 795; DB 4; Length 255;
Best Local Similarity 58.4%; Pred. No. 9.1e-63;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 59
DB 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 60
QY 60 NCNCRVACGYFRPKKFCSSSTHNAECIEGPHCLGPQCTRCEDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSMCEQDCKGQELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTP-AP 177

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-816-605-9

Query Match 55.7%; Score 795; DB 2; Length 255;
Best Local Similarity 58.4%; Pred. No. 9.1e-63;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 59
DB 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 60
QY 60 NCNCRVACGYFRPKKFCSSSTHNAECIEGPHCLGPQCTRCEDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSMCEQDCKGQELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTP-AP 177
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHFKQPKFKTTGAAQE 235
DB 178 AREPGHSPQIISFFLALTSTALLFLFLLTRFSVVKRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACRCRCPQEEGG 250
DB 238 EDGCSRFPPEEEGG 252

RESULT 15
US-09-006-353A-11
Sequence 11, Application US/09006353A
Patent No. 6261801
GENERAL INFORMATION:
APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

Query Match 55.7%; Score 795; DB 2; Length 255;
Best Local Similarity 58.4%; Pred. No. 9.1e-63;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 59
DB 1 MGNVCYVIVVLLVLCCKVAVONSCDNCQGTFC-RKYNPVCKSCPPSTFSSIGGQP 60
QY 60 NCNCRVACGYFRPKKFCSSSTHNAECIEGPHCLGPQCTRCEDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSMCEQDCKGQELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTP-AP 177

RESULT 20
US-09-623-545A-2
Sequence 2, Application US/09623545A
Patent No. 6627200
GENERAL INFORMATION:
APPLICANT: Merckle GmbH
TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE PROLIFERATION OF PERIPHERAL MONOCYTES
FILE REFERENCE: 30424-IUSMO
CURRENT APPLICATION NUMBER: US/09/623,545A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: EPO 98103859.9
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/EP99/01440
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-623-545A-2

Query Match 55.7%; Score 795; DB 4; Length 255;
Best Local Similarity 58.4%; Pred. No. 9.1e-63;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFPC-RKYNPVCKSCPPSTFSSIGGQP 59
DB 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFPC-RKYNPVCKSCPPSTFSSIGGQP 60
QY 60 NCNCRVAGYFRFKFCSTHNAECIEGFCGLGQCTRCCKDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKESSTNSAECDCCTPGFHCGLGAGCSMCEQDCRQGOELTKGCKDC 120
QY 120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVWSPSTTISVTPEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTPP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFVLKWKIRKFFPHIFKQPFKTTGAQE 235
DB 178 AREPGHSPQIISFFALTSTALLFLFLTLRFSVVKRGKLLYIFKQPFMRPVQTTOE 237

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: KWO5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-03965-8

QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFPC-RKYNPVCKSCPPSTFSSIGGQP 59
DB 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFPC-RKYNPVCKSCPPSTFSSIGGQP 60
QY 60 NCNCRVAGYFRFKFCSTHNAECIEGFCGLGQCTRCCKDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKESSTNSAECDCCTPGFHCGLGAGCSMCEQDCRQGOELTKGCKDC 120
QY 120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVWSPSTTISVTPEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTPP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFVLKWKIRKFFPHIFKQPFKTTGAQE 235
DB 178 AREPGHSPQIISFFALTSTALLFLFLTLRFSVVKRGKLLYIFKQPFMRPVQTTOE 237

RESULT 22
US-08-816-605-2
Sequence 2, Application US/08816605
Patent No. 5874240
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

RESULT 21
PCT-US96-03965-8
Sequence 8, Application PC/TUS9603965
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuul
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
STATE: NY
COUNTRY: USA
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
FILING DATE:

Query Match 55.7%; Score 795; DB 4; Length 255;
Best Local Similarity 58.4%; Pred. No. 9.1e-63;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFPC-RKYNPVCKSCPPSTFSSIGGQP 59
DB 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCPGTFPC-RKYNPVCKSCPPSTFSSIGGQP 60
QY 60 NCNCRVAGYFRFKFCSTHNAECIEGFCGLGQCTRCCKDCRPGQELTKGCKTC 119
DB 61 TCDICRQCKGVFRTRKESSTNSAECDCCTPGFHCGLGAGCSMCEQDCRQGOELTKGCKDC 120
QY 120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVWSPSTTISVTPEGGP 179
DB 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTPP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFVLKWKIRKFFPHIFKQPFKTTGAQE 235
DB 178 AREPGHSPQIISFFALTSTALLFLFLTLRFSVVKRGKLLYIFKQPFMRPVQTTOE 237

US-09-623-545A-2

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/816,605
 FILING DATE: 13-MAR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PR254
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8512
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 219 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-816-605-2

Query Match 45.9%; Score 656; DB 2; Length 219;
 Best Local Similarity 51.2%; Pred. No. 1.5e-50;
 Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;
 QY 1 MGNVCYVAVVILLVGCCKVAVQNSCDNCQPGTFCRKYNPVCSCPPSTFSSIGQPN 60
 DB 1 MGNVCYNVAVLLVLLVNLNPERTRSLQDPCSNCP----- 32
 QY 61 CNICRVACAGYFRFKFKSSSTNABCEIEGPHCLGPOCTRCCKDCRPGQELTKGCKTCS 120
 DB 33 -----AGVFRTRKESSTNABCECDCTPGPHCLGAGCSMCEQDCQKQELTKGCKDCC 85
 QY 121 LGTNDQNGTGVCRPWTNCSLDGRSVLTKGTETKDVVCGPPVVSFSTTISVTPGGPG 180
 DB 86 FGTNDQK-RGICRPWTNCSLDGRSVLTKGTETKDVVCGPPVVSFSTTISVTPPP-APA 142
 QY 181 ---GHSLOVLFALTS-ALLALIFITLFSVLKWRKFFHFKPPKKTGAAQEE 236
 DB 143 REPHSPQIIIFLALSTALLFILFLTRFSVVKGRKKLLYIFKQPMRPVQTQEE 202
 QY 237 DACSCRPQEEGG 250
 DB 203 DGCSCRPPEEEGG 216

RESULT 23
 US-09-523-323-55
 ; Sequence 55, Application US/09523323
 ; Patent No. 6635743
 ; GENERAL INFORMATION:
 ; APPLICANT: Ebner, Reinhard
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Ruben, Steven M.
 ; APPLICANT: Ullrich, Stephen
 ; APPLICANT: Zhai, Yifan
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
 ; FILE REFERENCE: 1488.065000C
 ; CURRENT APPLICATION NUMBER: US/09/523,323
 ; CURRENT FILING DATE: 2000-03-10
 ; EARLIER APPLICATION NUMBER: 60/168,380
 ; EARLIER FILING DATE: 1999-12-02
 ; EARLIER APPLICATION NUMBER: 60/148,326
 ; EARLIER FILING DATE: 1999-08-11
 ; EARLIER APPLICATION NUMBER: 60/142,657
 ; EARLIER FILING DATE: 1999-07-06
 ; EARLIER APPLICATION NUMBER: 60/137,457
 ; EARLIER FILING DATE: 1999-06-04
 ; EARLIER APPLICATION NUMBER: 60/124,041
 ; EARLIER FILING DATE: 1999-03-11
 ; EARLIER APPLICATION NUMBER: 09/252,656
 ; EARLIER FILING DATE: 1999-02-19
 ; EARLIER APPLICATION NUMBER: 60/075,409

; EARLIER FILING DATE: 1998-02-20
 ; EARLIER APPLICATION NUMBER: 09/027,287
 ; EARLIER FILING DATE: 1998-02-20
 ; EARLIER APPLICATION NUMBER: 09/003,886
 ; EARLIER FILING DATE: 1998-01-07
 ; EARLIER APPLICATION NUMBER: 08/822,953
 ; EARLIER FILING DATE: 1997-03-21
 ; EARLIER APPLICATION NUMBER: 60/013,923
 ; EARLIER FILING DATE: 1996-03-22
 ; EARLIER APPLICATION NUMBER: 60/030,157
 ; EARLIER FILING DATE: 1996-10-31
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 55
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-523-323-55
 Query Match 34.8%; Score 497; DB 4; Length 132;
 Best Local Similarity 63.9%; Pred. No. 9.6e-37;
 Matches 85; Conservative 13; Mismatches 33; Indels 2; Gaps 2;
 QY 28 CDNCOPGTFGR-KYNPVCSCPPSTFSSIGQPNICRVACAGYFRFKFKSSSTNABCE 86
 DB 1 CENCAGTFCDWRNQICSPCPNPSFSSAGGQRTCDICRCKGVFRTRKESSTNABCE 60
 QY 87 CIEGPHCLGPOCTRCCKDCRPGQELTKGCKTCSLGTNDQNGTGVCRPWTNCSLDGRSV 146
 DB 61 CTPGPHCLGAGCSMCEQDCQKQELTKGCKDCCGFTENKQK-RGICRPWTNCSLDGRSV 119
 QY 147 LKTGTETKDVVCG 159
 DB 120 LVNGTRERDVRVCG 132

RESULT 24
 US-08-866-545-11
 ; Sequence 11, Application US/08866545
 ; Patent No. 6265535
 ; GENERAL INFORMATION:
 ; APPLICANT: Greene, Mark I.
 ; APPLICANT: Murali, Ramachandran
 ; APPLICANT: Takasaki, Wataru
 ; TITLE OF INVENTION: PEPTIDES AND PEPTIDE
 ; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
 ; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Pennie & Edmonds LLP
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/866,545
 ; FILING DATE: 30-MAY-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 009113-0004-999
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 69 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6265535e
 US-08-866-545-11

Query Match 18.8%; Score 268; DB 3; Length 69;
 Best Local Similarity 63.8%; Pred. No. 8.2e-17;
 Matches 44; Conservative 17; Indels 0; Gaps 0;

QY 44 CKSCPSTSSIGGQPNICRVAGYFRFKFCSTHNAECCEIEGHCILGPGQCTRCEK 103
 DB 1 CSPCPNFSFSSAGGQRTCDICRQCKGVFRTRKECSSTNAECDCTPGFHCLGAGCSMCEQ 60

QY 104 DCRPGQELT 112
 DB 61 DCKQGGELT 69

RESULT 25
 US-09-627-775-11
 Sequence 11, Application US/09627775
 Patent No. 6682739
 GENERAL INFORMATION:
 APPLICANT: Greene, Mark
 APPLICANT: Murali, Ramachandran
 APPLICANT: Aoki, Kazuhiro
 APPLICANT: Baron, Roland
 TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
 FILE REFERENCE: UPN3832
 CURRENT APPLICATION NUMBER: US/09/627,775
 PRIOR FILING DATE: 2000-07-28
 PRIOR FILING DATE: 1999-07-28
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 11
 LENGTH: 69
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-627-775-11

Query Match 18.8%; Score 268; DB 4; Length 69;
 Best Local Similarity 63.8%; Pred. No. 8.2e-17;
 Matches 44; Conservative 17; Indels 0; Gaps 0;

QY 44 CKSCPSTSSIGGQPNICRVAGYFRFKFCSTHNAECCEIEGHCILGPGQCTRCEK 103
 DB 1 CSPCPNFSFSSAGGQRTCDICRQCKGVFRTRKECSSTNAECDCTPGFHCLGAGCSMCEQ 60

QY 104 DCRPGQELT 112
 DB 61 DCKQGGELT 69

RESULT 26
 US-09-006-353A-6
 Sequence 6, Application US/09006353A
 Patent No. 6261801
 GENERAL INFORMATION:
 APPLICANT: WEI, YING-FEI
 APPLICANT: YU, GUO-LIANG
 APPLICANT: GENTZ, REINER
 APPLICANT: RUBEN, STEVEN
 TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:

ADDRESS: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/006,353A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BROOKES, ANDERS A
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PF341
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 415 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-006-353A-6

Query Match 16.6%; Score 237; DB 3; Length 415;
 Best Local Similarity 27.0%; Pred. No. 3.3e-13;
 Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;
 QY 28 CDNCQPGTF-----CRKYNPVCKSCPSTSSIGGQ-PNCNICRVAGYFRFKCF--CSS 79
 DB 59 CSRCPPGGEFVAVCSRQDVTCKTCHNSYHNHLSLSTQLCRCPDIVLGFESVAPCTS 118
 QY 80 THNAECCEIEGHC--LGPQCTRCEK-----CRPGQEL-----TKQCKTCSLGT- 124
 DB 119 DRKAECRCQPGMSCVYLDNECVHCEERLVCQPGTEAEVTDVMDVNCVCPKPGHFQ 178
 QY 125 NDQNGTGVCRPWTCNSLDGSRVLTGTETKDVVCGPPVWSFSPSTTISVTPEGGPGGHS 184
 DB 179 NTSSFRACQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
 QY 185 QVLTFLALTSALLALIFITLLFSVLKWR-----KFPFHFKQPKKTTGAAQEDAC 239
 DB 220 --AMLLAILLSLVFLIFTVL--ACAWMRHPSLCRKLGLTKR-----HPEGEESP 268
 QY 240 SCRCPQEE 247
 DB 269 PCAPRAD 276

RESULT 27
 US-09-573-986-6
 Sequence 6, Application US/09573986
 Patent No. 6455340
 GENERAL INFORMATION:
 APPLICANT: Wei, Ying-Fei
 APPLICANT: Ni, Jian
 APPLICANT: Gentz, Reiner
 APPLICANT: Ruben, Steven
 TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
 FILE REFERENCE: 1488.1280004
 CURRENT APPLICATION NUMBER: US/09/573,986
 CURRENT FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 415

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-6

Query Match      16.6%; Score 237; DB 4; Length 415;
Best Local Similarity 27.0%; Pred. No. 3.3e-13;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCPGPTF-----CRKYNPVKSCPFSTFSSIGQ-PNCNICRVACGYFRFKKF--CSS 79
DB 59 CSRCPGGEFVFAVCSRSQDTVCKTCHPNSYNHNHLSQCLCRPCDVLGLFEEVAPCTS 118
QY 80 THNAECIEGPHC--LGPQCTREKD-----CRGQEL-----TKQCKTCSLGTGTF- 124
DB 119 DRKAECRCQPMGMSVYLNECVHCEERLVLCPGTAEAVTDEIMDTVNCVCPKPGHFQ 178
QY 125 NDQGTGVCPRWTNCSLDGRSVLKTGTTEKDVVCGPPVWSPSPSTTISVTPEGGPGHSL 184
DB 179 NTSSPRACQHTREICQGLVEAPGTSYSDTICKNP-----PEFG----- 219
QY 185 QVLTFLALTSALLLALIFITLLSVLKWIR-----KKFPHIFKQPKTKTTGAQBEDAC 239
DB 220 --AMLLALLSLVFLFTTVL--ACAWMRHPSLCRKLGTLLKR-----HPEGEESP 268
QY 240 SCRCPOEE 247
DB 269 PCPAPRAD 276

RESULT 28
US-08-996-139-15
; Sequence 15, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-15

Query Match      15.1%; Score 215; DB 3; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCPGPTF--CRKYNP-----VCKSCPPGTF--SSIGGQPNICRVACGYFRFKFCSSTH 81
DB 48 CSRCPGKYLKSCKTFTSDSVCLPCGPDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECEIEGPH-----CLGPQCTREKDCRPG-----QBLTKQG--CKTCSLGTGTFNDQ- 127
DB 108 TAPRECACTAGYHMNSDC---ECCRRNTECAPGFGCAQHPLQLNKDVTCTPCLLGGFFSDVF 164
QY 128 NCTGVCPRWTNCSLDGRSVLKTGTTEKDVVCGPPVWSPSPSTTISVTP--EGGPGHSLQV 186
DB 165 STDCKCKPWTNCTLLGKLEAHQGITPESDVVC-----SSMTLRPPKPEAQAYLPSLIV 217
QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKQPKTKTTGAQBEDA 238
DB 218 LLLFISV--VVVAIIFGVYRKSGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 29
US-08-995-659-15
; Sequence 15, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A

```


TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-15

Query Match 15.1%; Score 215; DB 3; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CONCPQTF-CRKYNP-----VCKSCPSTF-SSIGQPNICRVCAGYFRFKFCSTH 81
DB 48 CSRCEGKYLSSKCTPTSDVCLPCGDEYLDTWNEEDKLLHKVCDAGKALVADPGNH 107
QY 82 NA--ECCEIEGFH-----CLGPQCTCEKDCRPG-----OELTKQG-CKTCSLGTNDQ- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRNTECAPGFGAHPQLNKTCTCTCLLGFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186
DB 165 SSTDKCKPWTNCTLLGLEAHQGTTESDVVC-----SSMTLRPPKEAQYLP SLIV 217
QY 187 LTLFLALTSALLALIF-----ITLFSVLKWKIRKPPHIFKQPKFTTGAQAQBEDA 238
DB 218 LLLFISV-VVVAALIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 30

US-09-215-649A-15
Sequence 15, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

Query Match 15.1%; Score 215; DB 3; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKYNP-----VCKSCPSTF-SSIGQPNICRVCAGYFRFKFCSTH 81
DB 48 CSRCEGKYLSSKCTPTSDVCLPCGDEYLDTWNEEDKLLHKVCDAGKALVADPGNH 107
QY 82 NA--ECCEIEGFH-----CLGPQCTCEKDCRPG-----OELTKQG-CKTCSLGTNDQ- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRNTECAPGFGAHPQLNKTCTCTCLLGFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186
DB 165 SSTDKCKPWTNCTLLGLEAHQGTTESDVVC-----SSMTLRPPKEAQYLP SLIV 217
QY 187 LTLFLALTSALLALIF-----ITLFSVLKWKIRKPPHIFKQPKFTTGAQAQBEDA 238
DB 218 LLLFISV-VVVAALIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 31

US-09-577-780-15
Sequence 15, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693

```
/ REFERENCE/DOCKET NUMBER: 2852-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 625 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15

Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKYNP-----VCKSCPSTF-SSIGQPNMNCVACGYFRFKFCSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKCLLHKVCDAGKALVADPGNH 107
QY 82 NA--ECECIEGFH---CLGPQCTRCCKDCRPG-----QBLTKQG-CKTCSLGTFTNDQ- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVP 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSIQV 186
DB 165 SSTDKCKPWTNCTLLGKLEAHQGTESDVVC-----SSMTLRRPPKQAQYLP SLIV 217
QY 187 LTLFLALTSALLALIF-----ITLLFSVLKWKIRKPHIFKQPFKTTGAQAEEDA 238
DB 218 LLLFISV--VVAAIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 22
US-09-577-800-15
/ Sequence 15, Application US/09577800
/ Patent No. 6479635
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Dirk M.
/ APPLICANT: Galibert, Laurent
/ APPLICANT: Maraskovsky, Eugene
/ TITLE OF INVENTION: Receptor Activator of NF-kappaB
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation, Law Department
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: Apple Power Macintosh
/ SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/577,800
/ FILING DATE: 24-MAY-2000
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/996,139
/ FILING DATE: 22 DECEMBER 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 60/064,671
/ FILING DATE: 14 OCTOBER 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/813,509
/ FILING DATE: 07 MARCH 1997

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/772,330
/ FILING DATE: 23 DECEMBER 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2851-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 625 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-577-800-15

Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKYNP-----VCKSCPSTF-SSIGQPNMNCVACGYFRFKFCSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKCLLHKVCDAGKALVADPGNH 107
QY 82 NA--ECECIEGFH---CLGPQCTRCCKDCRPG-----QBLTKQG-CKTCSLGTFTNDQ- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVP 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSIQV 186
DB 165 SSTDKCKPWTNCTLLGKLEAHQGTESDVVC-----SSMTLRRPPKQAQYLP SLIV 217
QY 187 LTLFLALTSALLALIF-----ITLLFSVLKWKIRKPHIFKQPFKTTGAQAEEDA 238
DB 218 LLLFISV--VVAAIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 33
US-09-466-496-15
/ Sequence 15, Application US/09466496
/ Patent No. 6528482
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Dirk M.
/ APPLICANT: Galibert, Laurent
/ APPLICANT: Maraskovsky, Eugene
/ TITLE OF INVENTION: Receptor Activator of NF-kappaB
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation, Law Department
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: Apple Power Macintosh
/ SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/466,496
/ FILING DATE: 17-Dec-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/996,139
/ FILING DATE: 22 DECEMBER 1997
/ APPLICATION NUMBER: USSN 60/064,671
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;; FILING DATE: 14 OCTOBER 1997
;; APPLICATION NUMBER: USN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; APPLICATION NUMBER: USN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 625 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-466-496-15

Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPSTP-SSIGQPNICRCVAGYFRFKKCSSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECCEIEGFH----CLGPOCTRCCKDCRPG-----QELTKQG-CKTCSLGTFNDO- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164
QY 128 NGTGVCRPWTNCLDGRSVLKTGTTKDVVCGPPVVSFSTTISVTP-EGFGPGHSLQV 186
DB 165 SSTDKCKPWTNCTLLGLEAHQGTTESDVVC-----SSMTLRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLALIF-----ITLFSVLKWKIRKFPFHFKQPKKTTGAAQEEDA 238
DB 218 LLLFISV--VVVAALFGVYRKGKALTANLWNV-----NDA 254
QY 239 CSCRCPQEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 34
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871.856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/996,139
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: USN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; APPLICATION NUMBER: USN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 625 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPSTP-SSIGQPNICRCVAGYFRFKKCSSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECCEIEGFH----CLGPOCTRCCKDCRPG-----QELTKQG-CKTCSLGTFNDO- 127
DB 108 TAPRRCACTAGYHNSDC---ECCRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164
QY 128 NGTGVCRPWTNCLDGRSVLKTGTTKDVVCGPPVVSFSTTISVTP-EGFGPGHSLQV 186
DB 165 SSTDKCKPWTNCTLLGLEAHQGTTESDVVC-----SSMTLRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLALIF-----ITLFSVLKWKIRKFPFHFKQPKKTTGAAQEEDA 238
DB 218 LLLFISV--VVVAALFGVYRKGKALTANLWNV-----NDA 254
QY 239 CSCRCPQEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 35
US-09-871-291-15
; Sequence 15, Application US/09871291
; Patent No. 6562948
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,291
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-291-15

Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;
QY 28 CDNCPGTF-CKYNP-----VCKSCPSTF-SSIGGPNQNICRVACGYFRFKFCSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKLLHKVCDAGKALVADPGNH 107
QY 82 NA--ECECIEGFH---CLGPOCTRCEDCRPG-----OELTKQG-CKTCSLGTNDQ- 127
DB 108 TAPRCACATAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTCLLGGFSDVF 164
QY 128 NGTGVCRWNTCSLDGRSVLKTGTEKDVCGPPVSPSTTISVTP-EGGPGHSLQV 186
DB 165 SSTDKCKRWNTCTLLGLEAHQGTESDVC-----SSMTLRPPKQAQYVLSLIV 217
QY 187 LTLFLALTSALLALIF-----ITLFSVLKWKRPKPHIFKQPKKTTGAQBEDA 238
DB 218 LLLFISV--VVAAIFGVYKKGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 36
US-09-877-650-15
Sequence 15, Application US/09877650
Patent No. 6649164
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-877-650-15
Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;
QY 28 CDNCPGTF-CKYNP-----VCKSCPSTF-SSIGGPNQNICRVACGYFRFKFCSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKLLHKVCDAGKALVADPGNH 107
QY 82 NA--ECECIEGFH---CLGPOCTRCEDCRPG-----OELTKQG-CKTCSLGTNDQ- 127
DB 108 TAPRCACATAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTCLLGGFSDVF 164
QY 128 NGTGVCRWNTCSLDGRSVLKTGTEKDVCGPPVSPSTTISVTP-EGGPGHSLQV 186
DB 165 SSTDKCKRWNTCTLLGLEAHQGTESDVC-----SSMTLRPPKQAQYVLSLIV 217
QY 187 LTLFLALTSALLALIF-----ITLFSVLKWKRPKPHIFKQPKKTTGAQBEDA 238
DB 218 LLLFISV--VVAAIFGVYKKGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKESG 266

RESULT 37
US-09-041-886-27
Sequence 27, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-27

Query Match 14.6%; Score 208.5; DB 3; Length 276;
Best Local Similarity 25.7%; Pred. No. 7e-11;
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;

QY 18 CEKGVAVQNS--CDNCQPG-----TFCRKYNPV-CKSCPPSTP-SSIGGQPNICRVCAG 69
Db 26 CREKQYLNSQCCLQPGQKLVSDCTETETETECPLCGESEFLDTWNRETHCHQHKYCDP 85
QY 70 Y--FRFKKFCSSTHNAECIEGFCGLGPOCTRC--EKDCRPG-----QELTKQCKT 118
Db 86 NLGLRVQCKGTSETDTICTCEEGWHCTSEACSCVLHRSCTSPFGVQKIATGVSDTICEP 145
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
Db 146 CPVGFFSNVSSAFKCHPWTSCTETKDLVVQAGTKNTDVCVGPQ-----189
QY 178 GPGCHSLQVLTFLALTSALLALIFITLLFSVLKWKRFPHFKQPK-----K 228
Db 190 -DLRALVPIIFGLFALLVLFVFIK---KVAKPTNKAPHPKQEPQEIFNFPDDLPGS 245
QY 229 TTGAQAEEDACSCRCPOEEG 249
Db 246 NTAAPVQETLHGCPVTQEDG 266

RESULT 38
US-09-042-785A-10
Sequence 10, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-10

Query Match 14.6%; Score 208.5; DB 3; Length 277;
Best Local Similarity 25.7%; Pred. No. 7e-11;
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;

QY 18 CEKGVAVQNS--CDNCQPG-----TFCRKYNPV-CKSCPPSTP-SSIGGQPNICRVCAG 69
Db 26 CREKQYLNSQCCLQPGQKLVSDCTETETETECPLCGESEFLDTWNRETHCHQHKYCDP 85
QY 70 Y--FRFKKFCSSTHNAECIEGFCGLGPOCTRC--EKDCRPG-----QELTKQCKT 118
Db 86 NLGLRVQCKGTSETDTICTCEEGWHCTSEACSCVLHRSCTSPFGVQKIATGVSDTICEP 145
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
Db 146 CPVGFFSNVSSAFKCHPWTSCTETKDLVVQAGTKNTDVCVGPQ-----189
QY 178 GPGCHSLQVLTFLALTSALLALIFITLLFSVLKWKRFPHFKQPK-----K 228
Db 190 -DLRALVPIIFGLFALLVLFVFIK---KVAKPTNKAPHPKQEPQEIFNFPDDLPGS 245
QY 229 TTGAQAEEDACSCRCPOEEG 249
Db 246 NTAAPVQETLHGCPVTQEDG 266

RESULT 39
US-09-006-353A-10
Sequence 10, Application US/09006353A
Patent No. 6261801
GENERAL INFORMATION:
APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:40:42 ; Search time 94.6849 Seconds
(without alignments)
749.438 Million cell updates/sec

Title: US-10-067-122B-2
Perfect score: 1428
Sequence: 1 MGNNCYVNVVILLVGCCK.....DACSCRCQBERGGGGYIEL 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 27189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
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14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1428	100.0	256	13	US-10-027-199-10
2	1428	100.0	256	14	US-10-067-122-2
3	1085	76.0	131	11	US-09-405-032-136
4	795	55.7	255	9	US-09-739-394-9
5	795	55.7	255	9	US-09-826-212-11
6	795	55.7	255	9	US-09-935-727-13
7	795	55.7	255	10	US-09-877-336-2
8	795	55.7	255	13	US-10-097-330-9
9	795	55.7	255	13	US-10-027-199-2
10	795	55.7	255	14	US-10-170-997-2
11	795	55.7	255	14	US-10-186-643-11
12	795	55.7	255	14	US-10-207-655-160
13	795	55.7	255	15	US-10-418-242-13
14	656	45.9	219	9	US-09-739-394-2
15	656	45.9	219	13	US-10-097-330-2

16	497	34.8	132	15	US-10-375-680-55	Sequence 55, Appl
17	237	16.6	402	12	US-10-087-192-939	Sequence 539, Appl
18	237	16.6	415	9	US-09-826-212-6	Sequence 6, Appl
19	237	16.6	415	9	US-09-907-372-20	Sequence 20, Appl
20	237	16.6	415	9	US-09-935-727-8	Sequence 8, Appl
21	237	16.6	415	10	US-09-917-372-20	Sequence 20, Appl
22	237	16.6	415	14	US-10-186-643-6	Sequence 6, Appl
23	237	16.6	415	15	US-10-418-242-8	Sequence 8, Appl
24	215	15.1	625	9	US-09-871-856-15	Sequence 15, Appl
25	215	15.1	625	9	US-09-877-650-15	Sequence 15, Appl
26	215	15.1	625	12	US-09-865-363-15	Sequence 15, Appl
27	215	15.1	625	12	US-10-151-071-2	Sequence 2, Appl
28	215	15.1	625	12	US-09-957-944-4	Sequence 4, Appl
29	215	15.1	625	14	US-10-166-232A-2	Sequence 2, Appl
30	215	15.1	625	14	US-10-405-878-15	Sequence 15, Appl
31	214.5	15.0	277	9	US-09-839-339A-1	Sequence 1, Appl
32	212.5	14.9	276	15	US-10-369-300-4	Sequence 4, Appl
33	209.5	14.7	615	9	US-09-768-779A-2	Sequence 2, Appl
34	209.5	14.6	615	14	US-10-291-480-2	Sequence 10, Appl
35	208.5	14.6	277	9	US-09-826-212-10	Sequence 4, Appl
36	208.5	14.6	277	9	US-09-768-779A-4	Sequence 12, Appl
37	208.5	14.6	277	12	US-10-328-953-323	Sequence 323, Appl
38	208.5	14.6	277	14	US-10-291-480-4	Sequence 4, Appl
39	208.5	14.6	277	14	US-10-186-643-10	Sequence 10, Appl
40	208.5	14.6	277	15	US-10-418-242-12	Sequence 12, Appl
41	208.5	14.6	277	9	US-09-855-528-2	Sequence 2, Appl
42	207.5	14.5	622	12	US-09-957-944-10	Sequence 10, Appl
43	206	14.4	240	9	US-09-915-593-6	Sequence 6, Appl
44	205.5	14.4	240	14	US-10-283-105-6	Sequence 6, Appl
45	205.5	14.4	240	14	US-10-283-105-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-027-199-10
; Sequence 10, Application US/10027199
; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-027-199-10

Query Match	100.0%	Score 1428;	DB 13;	Length 256;
Best Local Similarity	100.0%;	Pred. No. 4.6e-119;	Mismatches 0;	Indels 0;
Matches 256;	Conservative	0;		Gaps 0;
QY	1	MGNNCYVNVVILLVGCCKVGVNSCDNCPQTFCKRYNPVCKSCPSTFSSIGGGPN	60	
Db	1	MGNNCYVNVVILLVGCCKVGVNSCDNCPQTFCKRYNPVCKSCPSTFSSIGGGPN	60	
QY	61	CNICRVCAGYFRFKFCSSTHNAECIEGHCJGPOCTRCKDCRPGOELTKGCKTCS	120	
Db	61	CNICRVCAGYFRFKFCSSTHNAECIEGHCJGPOCTRCKDCRPGOELTKGCKTCS	120	
QY	121	LGTFNDQNGTGVCRWTWNCISLDGRSVLXTGTTEKDVCGPPVSPSPSTTISVTPEGGFG	180	

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Db 121 LGTFNDQGTGCRPTWNCSDGRSVLKTGITERKDVVCGPPVVSFSTTISVTPEGGPG 180
QY 181 GHSLOVTLFLALTALLALIFITLLFSVLKWKIRKPPHIFKOPFKKTTGAAQEDACS 240
Db 181 GHSLOVTLFLALTALLALIFITLLFSVLKWKIRKPPHIFKOPFKKTTGAAQEDACS 240
QY 241 CRCPOEEGGGGYEL 256
Db 241 CRCPOEEGGGGYEL 256

RESULT 2
US-10-067-122-2
; Sequence 2, Application US/10067122
; Publication No. US20030100745A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/10/067,122
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 08/012,269
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-122-2

Query Match 100.0%; Score 1428; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 4.6e-119;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVWVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNNCYNVWVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVGAGYFRFKFSCSTHNAECEIEGFHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
Db 61 CNICRVGAGYFRFKFSCSTHNAECEIEGFHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
QY 121 LGTFNDQGTGCRPTWNCSDGRSVLKTGITERKDVVCGPPVVSFSTTISVTPEGGPG 180
Db 121 LGTFNDQGTGCRPTWNCSDGRSVLKTGITERKDVVCGPPVVSFSTTISVTPEGGPG 180
QY 181 GHSLOVTLFLALTALLALIFITLLFSVLKWKIRKPPHIFKOPFKKTTGAAQEDACS 240
Db 181 GHSLOVTLFLALTALLALIFITLLFSVLKWKIRKPPHIFKOPFKKTTGAAQEDACS 240
QY 241 CRCPOEEGGGGYEL 256
Db 241 CRCPOEEGGGGYEL 256

RESULT 3
US-09-405-032-136
; Sequence 136, Application US/09405032
; Publication No. US2003020782A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
```

```
STATE: California
COUNTRY: United States
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/405,032
APPLICATION NUMBER: US/09/405,032
FILING DATE: 24-Sep-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378-CIP2
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-405-032-136

Query Match 76.0%; Score 1085; DB 11; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVWVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNNCYNVWVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
QY 61 CNICRVGAGYFRFKFSCSTHNAECEIEGFHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
Db 61 CNICRVGAGYFRFKFSCSTHNAECEIEGFHCLGPOCTRCCKDCRPGQELTKQGCKTCS 120
QY 121 LGTFNDQGTGCRPTWNCSDGRSVLKTGITERKDVVCGPPVVSFSTTISVTPEGGPG 180
Db 121 LGTFNDQGTGCRPTWNCSDGRSVLKTGITERKDVVCGPPVVSFSTTISVTPEGGPG 180
QY 181 GHSLOVTLFL 191
Db 181 GHSLOVTLFL 191

RESULT 4
US-09-739-394-9
; Sequence 9, Application US/09739394
; Patent No. US20010014465A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Yu, Guo-Liang
; Gentz, Reiner
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,394
FILING DATE: 19-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
```


APPLICATION NUMBER: 09/253,549
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-739-394-9

Query Match 55.7%; Score 795; DB 9; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 59
Db 1 MGNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 60
QY 60 NCNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 119
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHLGAGCSMCEDCKQOGLTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTNDQK-RGICRPTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLALIFITLLFSVLKWKIRKPPHIFKQFFKTTGAAG 235
Db 178 AREPGHSPQIISFFLALTSTALLFLFLTFRLFSVVKRGRKLLYIFKQPPMRPVQTQ 237
QY 236 EDACSCRCPOEEGG 250
Db 238 EDGSCRCFPPEEGG 252

RESULT 5
US-09-826-212-11
Sequence 11, Application US/09826212
Patent No. US20010021516A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280006
CURRENT APPLICATION NUMBER: US/09/826,212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent in version 3.0
SEQ ID NO 11
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-212-11

Query Match 55.7%; Score 795; DB 9; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 59
Db 1 MGNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 60

QY 60 NCNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 119
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHLGAGCSMCEDCKQOGLTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTNDQK-RGICRPTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLALIFITLLFSVLKWKIRKPPHIFKQFFKTTGAAG 235
Db 178 AREPGHSPQIISFFLALTSTALLFLFLTFRLFSVVKRGRKLLYIFKQPPMRPVQTQ 237
QY 236 EDACSCRCPOEEGG 250
Db 238 EDGSCRCFPPEEGG 252

RESULT 6
US-09-935-727-13
Sequence 13, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/169,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 13
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-727-13

Query Match 55.7%; Score 795; DB 9; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;
QY 1 MGNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 59
Db 1 MGNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 60
QY 60 NCNVCYVAVVILLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGP 119
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHLGAGCSMCEDCKQOGLTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179

Db 121 CFGTNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGFSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSVLKWKRFPHIFKQPKKTTGAQE 235
Db 178 AREPGHSQIISFFLALTSTALLFLFLTLRFSVVKGRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEGG 250
Db 238 EDGCSCRFPBEEGG 252

RESULT 7

US-09-877-336-2
; Sequence 2, Application US/09877336
; Publication No. US20030000851A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHODS OF USING HUMAN RECEPTOR ON
; FILE REFERENCE: 740.011US3
; CURRENT APPLICATION NUMBER: US/09/877,336
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 09/007,097
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: 08/409,851
; PRIOR FILING DATE: 1995-03-23
; PRIOR APPLICATION NUMBER: 08/122,796
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-877-336-2

Query Match 55.7%; Score 795; DB 10; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62; Indels 8; Gaps 6;
Matches 149; Conservative 31; Mismatches 67

QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPQGTFC-RKYNPVCKSCPSTFSSIGGP 59
Db 1 MGNVCYNIVATLLVLNPFRTSLQDPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGQ 60
QY 60 NCNCRVCAGYFRFKFCSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTC 119
Db 61 TCDICRQCKGVFRTRKCSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEG 179
Db 121 CFGTNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGFSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSVLKWKRFPHIFKQPKKTTGAQE 235
Db 178 AREPGHSQIISFFLALTSTALLFLFLTLRFSVVKGRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEGG 250
Db 238 EDGCSCRFPBEEGG 252

RESULT 8

US-10-097-330-9
; Sequence 9, Application US/10097330
; Publication No. US20020127651A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
; FILE REFERENCE: PF254D1C2
; CURRENT APPLICATION NUMBER: US/10/097,330
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/739,394
; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 09/253,549
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: US 08/816,605
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 60/013,474
; PRIOR FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-330-9

Query Match 55.7%; Score 795; DB 13; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62; Indels 8; Gaps 6;
Matches 149; Conservative 31; Mismatches 67

QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPQGTFC-RKYNPVCKSCPSTFSSIGGP 59
Db 1 MGNVCYNIVATLLVLNPFRTSLQDPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGQ 60
QY 60 NCNCRVCAGYFRFKFCSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTC 119
Db 61 TCDICRQCKGVFRTRKCSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEG 179
Db 121 CFGTNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGFSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSVLKWKRFPHIFKQPKKTTGAQE 235
Db 178 AREPGHSQIISFFLALTSTALLFLFLTLRFSVVKGRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEGG 250
Db 238 EDGCSCRFPBEEGG 252

RESULT 9

US-10-027-199-2
; Sequence 2, Application US/10027199
; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-199-2

Query Match 55.7%; Score 795; DB 13; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62; Indels 8; Gaps 6;
Matches 149; Conservative 31; Mismatches 67

QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPQGTFC-RKYNPVCKSCPSTFSSIGGP 59
Db 1 MGNVCYNIVATLLVLNPFRTSLQDPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGQ 60
QY 60 NCNCRVCAGYFRFKFCSSTHNAECIEGPHCLGPOCTCEKDCRPGQELTKGCKTC 119

Db 61 TCDICRQCKGVFRTRKESSTNAECDCCTPGFCHCLGAGSCNCEQCKQGOELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLFSVLKWKIRKFPKPKKTTTGAQOE 235
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVRGRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEEGG 250
Db 238 EDGCSRCRFPPEEEGG 252

RESULT 10
US-10-170-997-2
; Sequence 2, Application US/10170997
; Publication No. US20030082157A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: New Receptor and Related Products and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/170,997
; FILING DATE: 12-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,573
; FILING DATE: 22-OCT-1997
; APPLICATION NUMBER: 08/460,976
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 13-SEP-1993
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; APPLICATION NUMBER: US 08/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KWO4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-170-997-2

Query Match 55.7%; Score 795; DB 14; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGP 59
Db 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGP 60
QY 60 NNCIRVCAGVFRFKKPCSSSTHNAECIEGHCILGPOCTCEKDCRPGOELTKGCKTC 119
Db 61 TCDICRQCKGVFRTRKESSTNAECDCCTPGFCHCLGAGSCNCEQCKQGOELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLFSVLKWKIRKFPKPKKTTTGAQOE 235
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVRGRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEEGG 250
Db 238 EDGCSRCRFPPEEEGG 252

RESULT 11
US-10-186-643-11
; Sequence 11, Application US/10186643
; Publication No. US20030118546A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/10/186,643
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-643-11

Query Match 55.7%; Score 795; DB 14; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGP 59
Db 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGP 60
QY 60 NNCIRVCAGVFRFKKPCSSSTHNAECIEGHCILGPOCTCEKDCRPGOELTKGCKTC 119
Db 61 TCDICRQCKGVFRTRKESSTNAECDCCTPGFCHCLGAGSCNCEQCKQGOELTKGCKDC 120
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLFSVLKWKIRKFPKPKKTTTGAQOE 235
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVRGRKKLLYIFKQPFMRPVQTTQE 237
QY 236 EDACSCRCPOEEEGG 250
Db 238 EDGCSRCRFPPEEEGG 252

RESULT 12
US-10-207-655-160
; Sequence 160, Application US/10207655

```
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 160
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-160

Query Match      55.7%; Score 795; DB 14; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNKCNVNVVILLVGGCKVAVQNSCDNCPGTFEC-RKYNPVCKSCPPSTFSSIGGQP 59
Db 1 MGNKCNVNVVILLVGGCKVAVQNSCDNCPGTFEC-RKYNPVCKSCPPSTFSSIGGQP 59
QY 60 NCNCRVAGYFRFKFSCSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKGCKTC 119
Db 61 TCDICRQCKGVFRTRKECSSTNAECDCCTPGFHLGAGCSMCEQDCKQGLTKGCKDC 120
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGP 179
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHIFKOPPKTTGAQAE 235
Db 178 AREPGHSQIISFFLALTSALLFLFLTLRFSVVKGRKLLYIFKOPFMRPVQTQAE 237
QY 236 EDACSCRCRQEBEGG 250
Db 238 EDGCSRCRFPPEEGG 252

RESULT 13
; Sequence 13, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P3
; CURRENT APPLICATION NUMBER: US/10/418,242
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,604
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,279
; PRIOR FILING DATE: 1999-04-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 51
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; SEQ ID NO 13
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-13

Query Match      55.7%; Score 795; DB 15; Length 255;
Best Local Similarity 58.4%; Pred. No. 1e-62;
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNKCNVNVVILLVGGCKVAVQNSCDNCPGTFEC-RKYNPVCKSCPPSTFSSIGGQP 59
Db 1 MGNKCNVNVVILLVGGCKVAVQNSCDNCPGTFEC-RKYNPVCKSCPPSTFSSIGGQP 59
QY 60 NCNCRVAGYFRFKFSCSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKGCKTC 119
Db 61 TCDICRQCKGVFRTRKECSSTNAECDCCTPGFHLGAGCSMCEQDCKQGLTKGCKDC 120
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGP 179
Db 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGP 179
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHIFKOPPKTTGAQAE 235
Db 178 AREPGHSQIISFFLALTSALLFLFLTLRFSVVKGRKLLYIFKOPFMRPVQTQAE 237
QY 236 EDACSCRCRQEBEGG 250
Db 238 EDGCSRCRFPPEEGG 252

RESULT 14
US-09-739-394-2
; Sequence 2, Application US/09739394
; Patent No. US20010014465A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Yu, Guo-Liang
; Gentz, Reiner
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,394
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/253,549
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-739-394-2
Query Match 45.9%; Score 656; DB 9; Length 219;
Best Local Similarity 51.2%; Pred. No. 2.1e-50;
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;

QY 1 MGNVCYVIVLLVGEKVGAVQNSCDNCPGTFCKYKYNPVCKSCPPSTFSSIGGQPN 60
DB 1 MGNVCYVIVLLVGEKVGAVQNSCDNCPGTFCKYKYNPVCKSCPPSTFSSIGGQPN 32
QY 61 CNICRVACGYVFRKFCSTHNAECIEGPHCLGPGQTRCEKDCRPGQELTKGCKTCS 120
DB 33 -----AGVFRTRKESSTNAECDCTPGFHLGAGCSMCEODCKQGOELTKGCKDCC 85
QY 121 LGTFNDQNGTGVCRPWNCSLGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
DB 86 FGTENDQK-RGICRPWNCSLGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 142
QY 181 ---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFPKFFKPKTTGAAQBE 236
DB 143 REPQHSQIIISFFLALTSTALLFLFLTRFVWGRKKLLYIFKQFMRPVQTTQEE 202
QY 237 DACSCRCPOEEGG 250
DB 203 DGSCRCFPPEEEGG 216

RESULT 15

US-10-097-330-2
Query Match 45.9%; Score 656; DB 13; Length 219;
Best Local Similarity 51.2%; Pred. No. 2.1e-50;
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
FILE REFERENCE: PF254D1C2
CURRENT APPLICATION NUMBER: US/10/097,330
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/739,394
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/253,549
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: US 08/816,605
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 60/013,474
PRIOR FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent in version 3.1
SEQ ID NO 2
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-330-2

QY 1 MGNVCYVIVLLVGEKVGAVQNSCDNCPGTFCKYKYNPVCKSCPPSTFSSIGGQPN 60
DB 1 MGNVCYVIVLLVGEKVGAVQNSCDNCPGTFCKYKYNPVCKSCPPSTFSSIGGQPN 32
QY 61 CNICRVACGYVFRKFCSTHNAECIEGPHCLGPGQTRCEKDCRPGQELTKGCKTCS 120
DB 33 -----AGVFRTRKESSTNAECDCTPGFHLGAGCSMCEODCKQGOELTKGCKDCC 85
QY 121 LGTFNDQNGTGVCRPWNCSLGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
DB 86 FGTENDQK-RGICRPWNCSLGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 142
QY 181 ---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFPKFFKPKTTGAAQBE 236
DB 143 REPQHSQIIISFFLALTSTALLFLFLTRFVWGRKKLLYIFKQFMRPVQTTQEE 202

QY 237 DACSCRCPOEEGG 250
DB 203 DGSCRCFPPEEEGG 216
RESULT 16
US-10-375-680-55
Query Match 34.8%; Score 497; DB 15; Length 132;
Best Local Similarity 63.9%; Pred. No. 1.7e-36;
Matches 85; Conservative 13; Mismatches 33; Indels 2; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000E
CURRENT APPLICATION NUMBER: US/10/375,680
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,234
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent in version 3.2
SEQ ID NO 55
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-375-680-55

QY 28 CDNCPGTFCKR-KYNPVCKSCPPSTFSSIGGQPNCRVCGYFRFKFKCSSTHNAECE 86
DB 1 CSNCPAGTFCDDNENQICSPCPNPSFSSAGGQRTCDICROCKGVFRTRKESSTNAECD 60
QY 87 CIEGFHCLGPGQTRCEKDCRPGQELTKGCKTCSLGTENDQNGTGVCRPWNCSLGRSV 146
DB 61 CTPGFHCLGAGCSMCEODCKQGOELTKGCKDCCFGTFNKOK-RGICRPWNCSLGRSV 119
QY 147 LKGTTEKDVVCG 159
DB 120 LVNGTKERDVVCG 132

RESULT 17

US-10-087-192-939
Query Match 16.6%; Score 237; DB 12; Length 402;
Best Local Similarity 27.0%; Pred. No. 8.5e-13;
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 939
LENGTH: 402
TYPE: PRT
ORGANISM: Mus musculus
US-10-087-192-939

Db 179 NTSSPRARCPHTRCEIOGLVEAAPTGSYSDTICKNP-----PEPG----- 219
QY 185 QVLTFLFALTSAALLALIFITLLFSLVKWIR-----KKFPHIFKQPKKTTGAAQEDAC 239
Db 220 --AMLLAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGLTLKR-----HPEGES 268
QY 240 SCRCPOEE 247
Db 269 PCPAPRAD 276

RESULT 22
US-10-186-643-6
; Sequence 6, Application US/10186643
; Publication No. US20030118546A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Bei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/10/186,643
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-643-6

Query Match 16.6%; Score 237; DB 14; Length 415;
Best Local Similarity 27.0%; Pred. No. 8.9e-13;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;
QY 28 CDNCPGTF-----CRKYNPVCKSPPTFSSIGGQ-PNCNICRVACAGYFRFKKF--CSS 79
Db 59 CSRCPPGFVFAVCSRSQDTVCKTCPHNSYNEHWNHLSLTCQLCRPCDIVLGFVEVAPCTS 118
QY 80 THNAECIEGPHC--LGPQCTRCED-----CRPQEL-----TKQCKTCSLGTG- 124
Db 119 DRKAECRCQPGMVCVYLDNECHVEERLVLCPQGTAEVDEIMDVTNVCVCPKPGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVWSFSPSTTISVTPEGGPGHSL 184
Db 179 NTSSPRARCPHTRCEIOGLVEAAPTGSYSDTICKNP-----PEPG----- 219
QY 185 QVLTFLFALTSAALLALIFITLLFSLVKWIR-----KKFPHIFKQPKKTTGAAQEDAC 239
Db 220 --AMLLAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGLTLKR-----HPEGES 268
QY 240 SCRCPOEE 247
Db 269 PCPAPRAD 276

RESULT 23
US-10-418-242-8
; Sequence 8, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454F3
; CURRENT APPLICATION NUMBER: US/10/418,242
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,604
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/935,727
; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-8

Query Match 16.6%; Score 237; DB 9; Length 415;
Best Local Similarity 27.0%; Pred. No. 8.9e-13;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;
QY 28 CDNCPGTF-----CRKYNPVCKSPPTFSSIGGQ-PNCNICRVACAGYFRFKKF--CSS 79
Db 59 CSRCPPGFVFAVCSRSQDTVCKTCPHNSYNEHWNHLSLTCQLCRPCDIVLGFVEVAPCTS 118
QY 80 THNAECIEGPHC--LGPQCTRCED-----CRPQEL-----TKQCKTCSLGTG- 124
Db 119 DRKAECRCQPGMVCVYLDNECHVEERLVLCPQGTAEVDEIMDVTNVCVCPKPGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVWSFSPSTTISVTPEGGPGHSL 184
Db 179 NTSSPRARCPHTRCEIOGLVEAAPTGSYSDTICKNP-----PEPG----- 219
QY 185 QVLTFLFALTSAALLALIFITLLFSLVKWIR-----KKFPHIFKQPKKTTGAAQEDAC 239
Db 220 --AMLLAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGLTLKR-----HPEGES 268
QY 240 SCRCPOEE 247
Db 269 PCPAPRAD 276

RESULT 21
US-09-917-372-20
; Sequence 20, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No. US20030068619A1 5600223
US-09-917-372-20

Query Match 16.6%; Score 237; DB 10; Length 415;
Best Local Similarity 27.0%; Pred. No. 8.9e-13;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;
QY 28 CDNCPGTF-----CRKYNPVCKSPPTFSSIGGQ-PNCNICRVACAGYFRFKKF--CSS 79
Db 59 CSRCPPGFVFAVCSRSQDTVCKTCPHNSYNEHWNHLSLTCQLCRPCDIVLGFVEVAPCTS 118
QY 80 THNAECIEGPHC--LGPQCTRCED-----CRPQEL-----TKQCKTCSLGTG- 124
Db 119 DRKAECRCQPGMVCVYLDNECHVEERLVLCPQGTAEVDEIMDVTNVCVCPKPGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVWSFSPSTTISVTPEGGPGHSL 184

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; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,279
; PRIOR FILING DATE: 1999-04-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 8
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-8

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Query Match 16.6%; Score 237; DB 15; Length 415;
Best Local Similarity 27.0%; Pred. No. 8.9e-13;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCQPGTF-----CRKYNVCKSPSTFSSIGSQ-FNCNCRVCACGYEFKFE--CSS 79
Db 59 CSRCPPGFVFVAVCSRSQDTVCKTCHNSYHWHNLSTCQLCRPCDVLVGFEEVAPCTS 118
QY 80 THNABCECIEGHC--LGPQCTRCBD-----CRPQCEL-----TKQGCKTCSLGTFF- 124
Db 119 DRKACRCQPGMCSVYLDNECVHCEERLVLCPQGTAEVTDIMTDVNCVCKPGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVWSPSTTISVTPPEGPGHSL 184
Db 179 NTSSPRACQPHTRCEIQGLVEAPGTSYDTCKNP-----PEPG----- 219
QY 185 QVTLFLALTSALLLALIFITLLFSVLKWR-----KFPFHIFKQPKKTTGAQAQEDAC 239
Db 220 --AMLLAILSLVFLFTTVL--ACAWMHPSLCRLKGLTKR-----HPEGES 268
QY 240 SCRCQEE 247
Db 269 PCPAPRAD 276

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RESULT 24
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; City: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856

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; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

Query Match 15.1%; Score 215; DB 9; Length 625;
Best Local Similarity 28.6%; Pred. No. 1.3e-10;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKYNP-----VCKSCPPSTF-SSIGQPNCRVCACGYEFKFCSTH 81
Db 48 CSRCPEKYLKCTPTSDSVCLPCGPDVYLTWNEEDKLLHVKDAGKALVAVDPGNH 107
QY 82 NA--ECCETEGH---CLGPOCTCEKDCRG-----OELTKG-CVTKSLGTNDQ- 127
Db 108 TAPRCACATAGHWSDC---ECCRRTECAPGQAQHPQLQNKDVTCTCLLGFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVWSPSTTISVTP-EGGPGHSLQV 186
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTESDVVC-----SSWTLRRPKQAQYLP SLIV 217
QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWRKKFPHIFKQPKKTTGAQAQED 238
Db 218 LLLFLISV--VVAAIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSRCQPEBEGG 250
Db 255 CSLSGNKESG 266

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RESULT 25
US-09-877-650-15
; Sequence 15, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; City: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-877-650-15

Query Match 15.1%; Score 215; DB 9; Length 625;
Best Local Similarity 28.6%; Pred. No. 1.3e-10;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VKSCPPSTP-SSIGGQPNICRVCAGYFRFKFCSSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECCEIEGFH-----CLGPOCTREKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127
DB 108 TAPRCACACTAGYHWNDC---ECCRNTECAPGFGAHPQLNKDVTCTCLLGFFSDVF 164
QY 128 NGTGVCRWTCNSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGHSLQV 186
DB 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLALIF-----ITLLFSVLKWKRPKFPKFPKTTGAAQEBDA 238
DB 218 LLLFISV--VVAAIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKSSG 266

RESULT 26
US-09-865-363-15
Sequence 15 Application US/09865363
Publication No. US20020086828A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,363
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-865-363-15

Query Match 15.1%; Score 215; DB 12; Length 625;
Best Local Similarity 28.6%; Pred. No. 1.3e-10;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VKSCPPSTP-SSIGGQPNICRVCAGYFRFKFCSSTH 81
DB 48 CSRCEPGKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECCEIEGFH-----CLGPOCTREKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127
DB 108 TAPRCACACTAGYHWNDC---ECCRNTECAPGFGAHPQLNKDVTCTCLLGFFSDVF 164
QY 128 NGTGVCRWTCNSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGHSLQV 186
DB 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLALIF-----ITLLFSVLKWKRPKFPKFPKTTGAAQEBDA 238
DB 218 LLLFISV--VVAAIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEGG 250
DB 255 CSSLSGNKSSG 266

RESULT 27
US-10-151-071-2
Sequence 2 Application US/10151071
Publication No. US20030017151A1
GENERAL INFORMATION:
APPLICANT: DOUGALL, William
APPLICANT: ANDERSON, Dirk
TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
FILE REFERENCE: 3277-A
CURRENT APPLICATION NUMBER: US/10/151,071
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/291,919
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 625
TYPE: PRT
ORGANISM: Mus musculus
US-10-151-071-2


```

18 CEKVGVQVNS---CDNQCPG---TFCKYKNPV-CKSCPPTF-SSIGGPPNCNCRVCAG 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
26 CREKQYLINSQCCLSQCPQKLVKDCDTEFETETECFLCGESEFLTDWRETHCHQHXYCDP 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
70 Y--FREKFKTCSSTHNAECIEGHCLGPQCTR--EKDCRPG-----QELTKQGCCT 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
86 NLGLRVQQXGTSFTDITICTCEGWHCTSEACSVLHRSCSGFGVKQJATGVSDTICEP 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 CSLGTENDONGT-VCRPTNCSLDGRSVLKTGTIEKVDKVGPPVVSFSPSTIISVTPEG 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
146 CPVGFFSNSSAGEKCHPWTSCTEKDLVQQAGTNKTDVVCQG-----189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
178 GPGGHSQWLVTPLAATSLALLALIPITLFLSVLKWIRKKFPHIFKOPFK-----K 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
190 -DLRALVVIPIFGILFALLVLVPIK---KVAKPTNKAPHPKQEPQOINFPDDLPGS 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
229 TTGAQOEEDACSCRCQPEEG 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
246 NTAAPVCRTLHGCPVTFQDG 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 32
 US-10-369-300-4
 ; Sequence 4, Application US/10369300
 ; Publication No. US20030215442A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraser, Christopher
 ; APPLICANT: Hancock, Wayne
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
 ; TITLE OF INVENTION: IMMUNE
 ; TITLE OF INVENTION: IMMUNE
 ; FILE REFERENCE: 7853-255
 ; CURRENT APPLICATION NUMBER: US/10/369,300
 ; CURRENT FILING DATE: 2003-02-19
 ; PRIOR APPLICATION NUMBER: 60/358,463
 ; PRIOR FILING DATE: 2002-02-19
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 276
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-369-300-4

[illegible]

RESULT 33
US-09-768-779A-2
; Sequence 2, Application US/09768779A

QY 178 GPGHSLQVLTFLALTSALLIALIFITLLSVLKWIRKPPHFKOPFK-----K 228
 Db 190 -DLRALVVIPIIFGILFAILLVLVFIK--KVAKPTNKAPHKQBPQEFNFFDDLPGS 245
 QY 229 TTGAQAEEDACSCRCPOEEG 249
 Db 246 NTAAPVQETLHGCPVTOEDG 266

RESULT 36
 US-09-768-779A-4
 ; Sequence 4, Application US/09768779A
 ; Patent No. US20020127637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JUAN
 ; MOORE, PAUL
 ; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
 ; RECEPTOR-LIKE PROTEIN 8
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09768,779A
 ; FILING DATE: 25-Jan-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/086,582
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KENLEY K. HOOVER
 ; REGISTRATION NUMBER: 40,302
 ; REFERENCE/DOCKET NUMBER: PF3668PP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8439
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 277 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-768-779A-4

Query Match 14.6%; Score 208.5; DB 9; Length 277;
 Best Local Similarity 25.7%; Pred. No. 1.9e-10;
 Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;
 QY 18 CEKVGAVQNS--CDNCQPG-----TFCRKYNPV-CKSCPPSTF-SSIGQPNMNCIRVCAG 69
 Db 26 CREKQYLNSQCCSLCQPGQKLVSDCTETETCLPCGESEFLDTWNRTHCHQHKYCDP 85
 QY 70 Y--FRFKFCSSTHNAECIEGPHCLGPOCTRC--EKDCRPG-----QELTKQCKT 118
 Db 86 NLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCTSPGFGVKIATGVSDTICEP 145
 QY 119 CSLGTF-NDQNGTGVCRPWNCSLDGRSVLKTGTETEDVYCGPPVWSFSPSTTISVTPEG 177
 Db 146 CPVGFPSNVSSAFKCHPWTSCTKDLVVQAGTKNTDVGCPQ-----189
 QY 178 GPGHSLQVLTFLALTSALLIALIFITLLSVLKWIRKPPHFKOPFK-----K 228
 Db 190 -DLRALVVIPIIFGILFAILLVLVFIK--KVAKPTNKAPHKQBPQEFNFFDDLPGS 245
 QY 229 TTGAQAEEDACSCRCPOEEG 249
 Db 246 NTAAPVQETLHGCPVTOEDG 266

Db 190 -DLRALVVIPIIFGILFAILLVLVFIK--KVAKPTNKAPHKQBPQEFNFFDDLPGS 245
 QY 229 TTGAQAEEDACSCRCPOEEG 249
 Db 246 NTAAPVQETLHGCPVTOEDG 266
 RESULT 37
 US-09-935-727-12
 ; Sequence 12, Application US/09935727
 ; Patent No. US20020150583A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
 ; FILE REFERENCE: PF454P2
 ; CURRENT APPLICATION NUMBER: US/09/935,727
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/303,224
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 60/252,131
 ; PRIOR FILING DATE: 2000-11-21
 ; PRIOR APPLICATION NUMBER: 60/227,598
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: 09/518,931
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/168,235
 ; PRIOR FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: 60/146,371
 ; PRIOR FILING DATE: 1999-08-02
 ; PRIOR APPLICATION NUMBER: 60/131,964
 ; PRIOR FILING DATE: 1999-04-30
 ; PRIOR APPLICATION NUMBER: 60/131,270
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/124,092
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/121,774
 ; PRIOR FILING DATE: 1999-03-04
 ; PRIOR APPLICATION NUMBER: 09/006,352
 ; PRIOR FILING DATE: 1998-01-13
 ; PRIOR APPLICATION NUMBER: 60/035,496
 ; PRIOR FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 277
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-935-727-12

Query Match 14.6%; Score 208.5; DB 9; Length 277;
 Best Local Similarity 25.7%; Pred. No. 1.9e-10;
 Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;
 QY 18 CEKVGAVQNS--CDNCQPG-----TFCRKYNPV-CKSCPPSTF-SSIGQPNMNCIRVCAG 69
 Db 26 CREKQYLNSQCCSLCQPGQKLVSDCTETETCLPCGESEFLDTWNRTHCHQHKYCDP 85
 QY 70 Y--FRFKFCSSTHNAECIEGPHCLGPOCTRC--EKDCRPG-----QELTKQCKT 118
 Db 86 NLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCTSPGFGVKIATGVSDTICEP 145
 QY 119 CSLGTF-NDQNGTGVCRPWNCSLDGRSVLKTGTETEDVYCGPPVWSFSPSTTISVTPEG 177
 Db 146 CPVGFPSNVSSAFKCHPWTSCTKDLVVQAGTKNTDVGCPQ-----189
 QY 178 GPGHSLQVLTFLALTSALLIALIFITLLSVLKWIRKPPHFKOPFK-----K 228
 Db 190 -DLRALVVIPIIFGILFAILLVLVFIK--KVAKPTNKAPHKQBPQEFNFFDDLPGS 245
 QY 229 TTGAQAEEDACSCRCPOEEG 249
 Db 246 NTAAPVQETLHGCPVTOEDG 266

RESULT 38
 US-10-328-953-323
 ; Sequence 323, Application US/10328953
 ; Publication No. US20040071656A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wieland, Felix
 ; APPLICANT: Hartl, Franz-Ulrich
 ; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
 ; FILE REFERENCE: 11390/46101
 ; CURRENT APPLICATION NUMBER: US/10/328,953
 ; CURRENT FILING DATE: 2002-12-23
 ; PRIOR APPLICATION NUMBER: US 60/342,570
 ; PRIOR FILING DATE: 2004-12-26
 ; PRIOR APPLICATION NUMBER: US 60/343,884
 ; PRIOR FILING DATE: 2001-12-28
 ; PRIOR APPLICATION NUMBER: US 60/372,620
 ; PRIOR FILING DATE: 2002-04-12
 ; PRIOR APPLICATION NUMBER: US 60/399,342
 ; PRIOR FILING DATE: 2002-07-29
 ; PRIOR APPLICATION NUMBER: US 60/414,834
 ; PRIOR FILING DATE: 2002-09-28
 ; NUMBER OF SEQ ID NOS: 331
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 323
 ; LENGTH: 277
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-328-953-323

Query Match 14.6%; Score 208.5; DB 12; Length 277;
 Best Local Similarity 25.7%; Pred. No. 1.9e-10;
 Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;
 QY 18 CEKVGAVONS--CDNCPG-----TFCRKNPV-CKSCPPSTF--SSIGQPNICRVACG 69
 Db 26 CREKYILNSQCCSLCQPGQKLVSDCTETETCLPCGESEFLDTWNRTHCHQHKYCDP 85
 QY 70 Y--FRFKKFCSTHNAECEIEGFHCLGPQCTRC--EKDCRPG-----QELTKQCKT 118
 Db 86 NLGLRVQOKGTSETDTICTCEGWHCTSEACSVLHRSCTSPGFGVKQIATGVSDTICEP 145
 QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSTTISVTPEG 177
 Db 146 CPVGFSSNVSAFAEKCHPWTSCETKDLVVQAGTKTDVWCGPQ-----189
 QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKQPFK-----K 228
 Db 190 -DLRALVWPIIFGILFAILLVLVFIK--KVAKPTNKAPHKQEPQEIINFDDLPGS 245
 QY 229 TTGAQAEEDACSCRCQPEEG 249
 Db 246 NTAAPVQETLHGCPVTQEDG 266

RESULT 39
 US-10-291-480-4
 ; Sequence 4, Application US/10291480
 ; Publication No. US20030100069A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Moore, Paul
 ; APPLICANT: Ni, Jian
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
 ; FILE REFERENCE: PF368C1D1
 ; CURRENT APPLICATION NUMBER: US/10/291,480
 ; CURRENT FILING DATE: 2002-11-12
 ; PRIOR APPLICATION NUMBER: 09/768,779
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/086,582
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/048,020
 ; PRIOR FILING DATE: 1997-05-29
 ; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 277
 ; TYPE: PRT
 ; ORGANISM: human
 US-10-291-480-4
 Query Match 14.6%; Score 208.5; DB 14; Length 277;
 Best Local Similarity 25.7%; Pred. No. 1.9e-10;
 Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;
 QY 18 CEKVGAVONS--CDNCPG-----TFCRKNPV-CKSCPPSTF--SSIGQPNICRVACG 69
 Db 26 CREKYILNSQCCSLCQPGQKLVSDCTETETCLPCGESEFLDTWNRTHCHQHKYCDP 85
 QY 70 Y--FRFKKFCSTHNAECEIEGFHCLGPQCTRC--EKDCRPG-----QELTKQCKT 118
 Db 86 NLGLRVQOKGTSETDTICTCEGWHCTSEACSVLHRSCTSPGFGVKQIATGVSDTICEP 145
 QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSTTISVTPEG 177
 Db 146 CPVGFSSNVSAFAEKCHPWTSCETKDLVVQAGTKTDVWCGPQ-----189
 QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKQPFK-----K 228
 Db 190 -DLRALVWPIIFGILFAILLVLVFIK--KVAKPTNKAPHKQEPQEIINFDDLPGS 245
 QY 229 TTGAQAEEDACSCRCQPEEG 249
 Db 246 NTAAPVQETLHGCPVTQEDG 266

RESULT 40
 US-10-186-643-10
 ; Sequence 10, Application US/10186643
 ; Publication No. US20030118546A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wei, Ying-Fei
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Gentz, Reiner
 ; APPLICANT: Ruben, Steven
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
 ; FILE REFERENCE: 1488.1280004
 ; CURRENT APPLICATION NUMBER: US/10/186,643
 ; CURRENT FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US/09/573,986
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 277
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-186-643-10

Query Match 14.6%; Score 208.5; DB 14; Length 277;
 Best Local Similarity 25.7%; Pred. No. 1.9e-10;
 Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;
 QY 18 CEKVGAVONS--CDNCPG-----TFCRKNPV-CKSCPPSTF--SSIGQPNICRVACG 69
 Db 26 CREKYILNSQCCSLCQPGQKLVSDCTETETCLPCGESEFLDTWNRTHCHQHKYCDP 85
 QY 70 Y--FRFKKFCSTHNAECEIEGFHCLGPQCTRC--EKDCRPG-----QELTKQCKT 118
 Db 86 NLGLRVQOKGTSETDTICTCEGWHCTSEACSVLHRSCTSPGFGVKQIATGVSDTICEP 145
 QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSTTISVTPEG 177
 Db 146 CPVGFSSNVSAFAEKCHPWTSCETKDLVVQAGTKTDVWCGPQ-----189
 QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKEPHIFKQPFK-----K 228

Db 190 -DLRALVVIPIIGILFAILLVLVFIK---KVAKKPTNKAPHKQEPQEIINFDDLPGS 245
QY 229 TTGAQBEDACSCRCPOEEG 249
Db 246 NTAAFPQETLHGCPVTQEDG 266

Search completed: May 5, 2004, 14:53:53
Job time : 96.6849 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:41 ; Search time 30.6849 Seconds
(without alignments)
802.512 Million cell updates/sec

Title: US-10-067-122B-2
Perfect score: 1428
Sequence: 1 MGNVCYVWVIVLLVGCXK.....DACSCRCPOEEGGGGYEL 256
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1428	100.0	256	2 B32393	T-cell antigen 4-1
2	795	55.7	255	2 I38426	lymphocyte activat
3	208.5	14.6	277	2 A60771	B-cell activation
4	202.5	14.2	277	2 I37552	OX40 homolog - hum
5	202	14.1	435	2 I54182	tumor necrosis fac
6	197	13.8	461	1 A35356	tumor necrosis fac
7	186.5	13.1	305	2 A46476	B cell-associated
8	185	13.0	474	2 B38634	tumor necrosis fac
9	182	12.7	459	2 I48854	gene murine tumour
10	173	12.1	651	2 JC7705	death receptor-6 -
11	170.5	11.9	271	2 S12783	OX40 antigen precu
12	169.5	11.9	250	1 A49053	CD27 antigen precu
13	166.5	11.7	260	1 A46517	CD27 antigen precu
14	158	11.1	272	2 I48700	gene ox40 protein
15	142	9.9	349	2 D72175	G2R protein - vari
16	140.5	9.8	325	2 B43692	T2 protein - rabbi
17	139.5	9.8	416	1 JN0006	nerve growth facto
18	138	9.7	348	2 T28623	hypothetical prote
19	138	9.7	349	2 T36858	gene G4R protein -
20	138	9.7	3106	1 S53868	laminin alpha-2 ch
21	135.5	9.5	713	2 A35502	major surface-labe
22	135	9.5	427	1 GQHUN	nerve growth facto
23	135	9.5	656	2 JC2005	integrin beta-5 ch
24	135	9.5	799	2 A38308	integrin beta-5 ch
25	133	9.3	425	1 A26431	nerve growth facto
26	130.5	9.1	326	1 GQVZML	T2 protein - myxom
27	129	9.0	1797	2 A55677	laminin beta-2 cha
28	129	9.0	3635	2 T10053	laminin alpha 5 ch
29	127	8.9	461	1 GQRTT1	tumor necrosis fac

ALIGNMENTS

RESULT 1

B32393
T-cell antigen 4-1BB precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: B32393; I48879
R:Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1983-1967, 1989
A:Title: cDNA sequence of two inducible T-cell genes.
A:Reference number: A32393; MUID:89184547; PMID:2784565
A:Accession: B32393
A:Molecule type: mRNA
A:Residues: 1-256 <KWO>
A:Cross-references: GS:J04492; NID:G201121; PIDN:AAA40167.1; PID:G201122
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 157, 2256-2262, 1994
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
A:Reference number: I48879; MUID:94179805; PMID:8133039
A:Accession: I48879
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-256 <RES>
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C:Genetics:
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 100.0%; Score 1428; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 4.8e-98;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGNVCYVWVIVLLVGCXKGVAVQNSCDNCQPGTFCRKYNPVCKSCPSTSSIGGQPN	60
DB	1	MGNVCYVWVIVLLVGCXKGVAVQNSCDNCQPGTFCRKYNPVCKSCPSTSSIGGQPN	60
QY	61	CNCRVAGYFRPKKFCSSSTHNAECIEGFHCLGQCTRCCKDCRPGQELTKQCKTCS	120
DB	61	CNCRVAGYFRPKKFCSSSTHNAECIEGFHCLGQCTRCCKDCRPGQELTKQCKTCS	120
QY	121	LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPGGPG	180
DB	121	LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPGGPG	180
QY	181	GHSIQVTLFLATSLALLALIFITLFSVLKWKIRKFKPKPKTKTGAQBEDACS	240
DB	181	GHSIQVTLFLATSLALLALIFITLFSVLKWKIRKFKPKPKTKTGAQBEDACS	240
QY	241	CRCPQEEGGGGYEL	256

heparan sulfate pr
laminin alpha-1 ch
tenascin-X - bovin
laminin beta-1 cha
subtilisin-like pr
laminin alpha-1 ch
laminin alpha-1 ch
laminin gamma-1 ch
hypothetical prote
hypothetical prote
probable laminin a
laminin gamma-1 ch
laminin beta-1 cha
hypothetical prote
protein T22A3.8 [1

A:Molecule type: mRNA
A:Residues: 1-461 <SMI>
A:Cross-references: GB:M32315; NID:G189185; PIDN:AAA5929.1; PID:G189186
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, P.C. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring
A:Reference number: A36475; MUID:91045991; PMID:2172983
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36755.1; PID:G339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Cytochrome 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690; PMID:1966549
A:Accession: A48416
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:G235648; PIDN:AAB19824.1; PID:G235649
A:Note: sequence extracted from NEB1 backbone (NCBIN:63368, NCBI:P:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of two distinct tumor necrosis factor receptors
A:Reference number: A36007; MUID:90349572; PMID:2166946
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GB:M35857; NID:G339751; PIDN:AAA63282.1; PID:G339752
R:Boetler, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.B.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors
A:Reference number: A23666; MUID:91056048; PMID:2173696
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>
R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct tumor necrosis factor receptors
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: B35010
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of the human TNF receptor
A:Reference number: I38094; MUID:95121934; PMID:7821811
A:Accession: I38094
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:G566044; PIDN:CAA56324.1; PID:G825701
C:Genetics
A:Gene: GDB:TNFR2
A:Cross-references: GDB:125914; OMIM:191191
A:Map position: lp36.2-lp36.2
A:Introns: 26/3
A:Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171, 193/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 197; DB 1; Length 461;
 Best Local Similarity 26.3%; Pred. No. 2.4e-07;
 Matches 72; Conservative 33; Mismatches 99; Indels 70; Gaps 15;

QY 25 QNSCDNCQPG-----TFCRK-YNPVCKSCPSTFSSI-GQPNCNIC-RVCAGYFRFKFC 77
 Db 51 QMCCSKSPGQAKVCTKTSITVDCSDSDSTYTQLNWVPECLSCGSRCSQDQVQAC 110
 QY 78 SSTHNAECSCIEGFHC-LGPO--CTRCE--KDCRQGLTKQG-----CKTSLGTF- 124
 Db 111 TREQNRICTRFGWYCALSKQGCRLCAPLRCRFGVGVARPTSTSDVCKPCAPGTF 170
 QY 125 NQNGTGVCRPWNCSLDGRSVLKTGTTEKDVVC----- 158
 Db 171 NTSSTDICRPHQICNV-----VAIPGNASMDAVCTSTPTSRMAPGAVHLPPQVSTRSQH 226
 QY 159 --GPPVWSPSTTI-----SVTEGGGGHSLQVLTFLALTSALLLALIFITLLFSV 210
 Db 227 TQTPTEPSTPSTFLLPMGPPPAEGSTGDFALPV-GLIVGVTAIGLLIIGVNCV--I 283
 QY 211 LKWIRK-----KPFHFQKPFKTTGAAQE 235
 Db 284 MTQVKKKPLCLQREAKVPHLPADKARGTQGPBQ 317

RESULT 7
 A46476
 B cell-associated surface molecule CD40, long splice form - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 A:Accession: A46476; A46515
 R:Torres, R.M.; Clark, E.A.
 J. Immunol. 148, 620-626, 1992
 A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine A46476
 A:Reference number: A46476; MUID:92105763; PMID:1370315
 A:Accession: A46476
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-305 <TOR>
 A:Cross-references: GB:M83312; NID:g1553058
 A>Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIIP:75207)
 A:Note: this translation is not annotated in GenBank entry M83312, release 113.0
 R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992
 A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
 A:Reference number: A46515; MUID:93094586; PMID:1281194
 A:Accession: A46515
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-287, 'LV' <GRI>
 A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
 A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIIP:75207)
 A:Experimental source: BALB/C, liver
 A:Note: sequence extracted from NCBI backbone (NCBIIP:120357)
 C:Comment: For an alternative splice form, see PIR:A46515.
 C:Comment: For an alternative splice form, see PIR:A46476.
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: alternative splicing; transmembrane protein
 F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 13.1%; Score 186.5; DB 2; Length 305;
 Best Local Similarity 25.1%; Pred. No. 1e-06;
 Matches 61; Conservative 34; Mismatches 87; Indels 61; Gaps 11;

QY 28 CDNCQPGTFCKRY-----NPVCKSCPSTFSSIGQP-NCNICRVACGY--PRFKFCSS 79
 Db 38 CDLCQPGSRSLTSHCTALEKTQCHPCDSGFSAQWNRIRCHQHRHCFNGLVKKEGTA 97
 QY 80 THNAECSCIEGFHCLGQCTCEK--DCRFG-----QLTKQGCKTCSLGTFFNQNGT 130
 Db 98 ESDTVCTCKGGQHTSKDCEACQHTPCIFGFMEMATETDTVCHPCFVGFFSQSSL 157
 QY 131 -GVCRPWNTNCSLDGRSVLKTGTTEKDVVCPPVVPVSPSTTISVTEPGGPGHSLQVLT 189

Db 158 FEKCPWTSCEKXNLEVLQKGTSTQTVICG-----L 188
 QY 190 FLAITSALLALI--FITLLFSVLKWKIRKFKPHFKQP--FKTTGAAQEEBACSCRCQ 245
 Db 189 KSMRALLVPPVVMGILITIFGVFLYIKR-----VVKPKDNEMLPPAARRQD-----BQ 238
 QY 246 EEE 248
 Db 239 EME 241

RESULT 8
 B38634
 tumor necrosis factor receptor type 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 27-Oct-2003
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor re
 A:Reference number: A38634; MUID:91187885; PMID:1849278
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEW>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t
 A:Reference number: A40254; MUID:91246168; PMID:1645445
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Kissoneghis, M.; Follows, R.; Feldmann, M.; Chernajovsky, Y.
 submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A:Reference number: S54816
 A:Accession: S54816
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-120/Domain: NGF receptor repeat homology <NG2>
 F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 13.0%; Score 185; DB 2; Length 474;
 Best Local Similarity 26.0%; Pred. No. 1.9e-06;
 Matches 75; Conservative 26; Mismatches 107; Indels 80; Gaps 15;

QY 25 QNSCDNCQPGT----FCRK-YNPVCKSCPSTFSSIGQPNCNICRVACGYFRFK----K 75
 Db 52 QMCCAKCPGQYVKHFCNKTSVTCADCEASMYQVWNQ---FRCLSCSSCTTDDQVEIR 109
 QY 76 FCSSTHNAECSCIEGFHCL-----GQCRCCKDCRPGQELTKQG-----CKTCSL 121
 Db 110 ACTQKNRVACACEAGRYCALKTHSGSCRCQMLSK-CGPGFGVASSRAPNGVNLCKACAP 168
 QY 122 GTFND-QNGTGVCRPWNCSLDGRSVLKTGTTEKDVVCGP--PVVSPSPSTTISVTP--- 175
 Db 169 GTFSTTSSDVCPRHICSI-----LAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPT 224
 QY 176 -----EGGP-----GHSLOVLTFLALTSALLLALIFITLL 207
 Db 225 RSQPLDQPGSPSTFSLTSLGSTFIIEQSTKGISLPI-GLIVGVTS---LGLMLGLV 280
 QY 208 FSVLKWIRKPKPHFKQPFKKTGAAQEEBACSCRCQEEBGGGGYE 255

Db 281 NCILVQRKKK-----SCLQDAKVPHPDEKSDAVGLE 316

RESULT 9

148854

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003

C:Accession: I48854

R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A:Reference number: I48854; MUID:95178648; PMID:7873884

A:Accession: I48854

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-459 <RES>

A:Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831

C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog

F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 12.7%; Score 182; DB 2; Length 459;

Best Local Similarity 26.6%; Pred. No. 3.1e-06;

Matches 75; Conservative 25; Mismatches 109; Indels 76; Gaps 15;

QY 25 QNSDCNCPQGT-----PCRK-YNPVCKSCPPSTFSSIGGO-PNCNIC-RVCAGYFRFKKFC 77

Db 37 QMCCAKCPFGQYVHKFCNKTSDTADCEASMYTQVMNQFRTCLSCSSCSCTDQVETRAC 96

QY 78 SSTHNAECIEGFHCL-----GPQCTRCCKDCRPGOELTKQG-----CKTCSLGT 123

Db 97 TKQNRVCAEAGRYALKTHSGSCQCKWLSK-CGPGFVASSRAPNGVLCACAPGT 155

QY 124 FND-QNGTGVCRPWNCSLDGRSVLTKGTTEKDVVCGP--PVVSPSPSTTISVTP----- 175

Db 156 FSDTTSSTDCVRPHRCSI-----LAIPGNASTDAVCAPESTLSAIPRTLYVSQPEPTRS 211

QY 176 -----EGGP-----GGHSLQVLTFLALTSALLALIFITLLFS 209

Db 212 QPLDQBPQPSQTSIITSLGSTPIIQSTKGGLSLPI-GLIVGTS-----LGLMLGLVNC 267

QY 210 VLKWRKKFPHIFKQPFKTTGAQAQBEDACSCRPQEEGGGGYE 255

Db 268 FILVQRKKK-----SCLQDAKVPHPDEKSDAVGLE 301

RESULT 10

JC7705

death receptor-6 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003

C:Accession: JC7705

R:Bridgman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A:Reference number: JC7705; MUID:21308433; PMID:11414698

A:Accession: JC7705

A:Molecule type: mRNA

A:Residues: 1-651 <BRI>

A:Cross-references: GB:AF349908

C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNFR family and activates a cell death and/or survival signaling cascade.

C:Genetics: 6

A:Gene: dr-6

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

F:1-21/Domain: signal sequence #status predicted <SIG>

F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F:332-350/Domain: transmembrane #status predicted <TM>

F:410-475/Domain: death domain #status predicted <DED>

F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 12.1%; Score 173; DB 2; Length 651;

Best Local Similarity 30.0%; Pred. No. 1.9e-05;

Matches 48; Conservative 22; Mismatches 72; Indels 18; Gaps 7;

QY 28 CDNCQPGTFCRKYNP-----VKSCPPSTFSS-IGQPNCNICR-VCAGYFRFKKFCST 80

Db 52 CDKCPAGTYVSKTKSTLRECPGPDGTFTKHENGIERCHPCPKCPCELPWIEKTHCTAL 111

QY 81 HNAECIEGFHCLGPGQCTCEKDCRPGOELTKQG-----CKTCSLGTEND-QNGTGV 132

Db 112 TDRECTCLSGTFQINDTCVPYTV-CPVGMGRKKGTETEDVRCKPCLGRGTFSDVPSSVMK 170

QY 133 CRPWNCSLDGRSVLTKGTTEKDVVCGPPVVFSPSTTIS 172

Db 171 CKTYTDCFGNMVVKVSGTKESDNCXSP--ASLPNTSLT 208

RESULT 11

S12783

OX40 antigen precursor - rat

N:Alternate names: nerve growth factor receptor homolog

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C:Accession: S12783; S08036

R:Maliet, S.; Fossum, S.; Barclay, A.N.

EMBO J. 9, 1063-1068, 1990

A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes

A:Reference number: S12783; MUID:90214614; PMID:2157591

A:Accession: S12783

A:Molecule type: mRNA

A:Residues: 1-271 <MAL>

A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: growth factor receptor; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-271/Product: OX40 antigen #status predicted <MAT>

F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 11.9%; Score 170.5; DB 2; Length 271;

Best Local Similarity 24.6%; Pred. No. 1.4e-05;

Matches 59; Conservative 19; Mismatches 83; Indels 79; Gaps 10;

QY 14 LLVGE-----KVGAVQNS-----CDNCQPG-----TFC-RKYNPVCKSCPPSTFSSIG 56

Db 12 LLLGLSLGVTKLNCVKDITYPSGHKCKRECQFGHGMVSRCDHTRTDVCHPCPEGFYNEAV 71

QY 57 GQPNCNICRVC--AGYFRFKFCSTHNAECIEG-----PHCLGPGQCTCEKDCRCP 107

Db 72 NYDTCKQCTQCNHRSGSELKQNTPTEDTVQCRPGTQPDSSHKLGVDCV-----PCPP 127

QY 108 GOELTKQCKTCSLGTENDQNGTGVCRPWNCSLDGRSVLTKGTTEKDVVCGP----- 160

Db 128 GH-----FSPGNSQACKPWTNCTLSGKQIRHPASNSLDTVCEDRSLLATL 172

QY 161 -----PVVSPSTTISVTPG-----GPGGHSLSQVLTFLAL 193

Db 173 LWETQRTTFRPTVPTVWRTSOLPSTPLVAPEGAPAVILGLGLLAFLLTLLAL 232

RESULT 12

A49053

CD27 antigen precursor - mouse

N:Alternate names: CD27L receptor; T cell activation antigen CD27

C:Species: Mus musculus (house mouse)

C:Date: 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_change 11-Sep-1998

C:Accession: A49053

R:Gravestein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp, P.; J. Immunol. 23, 943-950, 1993

A:Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte

A:Reference number: A49053; MUID:93209296; PMID:8384562

A:Accession: A49053

A:Molecule type: mRNA

A:Residues: 1-250 <GRA>

A:Note: sequence extracted from NCBI backbone (NCBI:128168; NCBI:128169)

C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-250/Product: CD27 antigen #status predicted <MAT>
F:21-182/Domain: extracellular #status predicted <EXT>
F:27-63/Domain: NGF receptor repeat homology <NG1>
F:65-105/Domain: NGF receptor repeat homology <NG2>
F:121-179/Region: proline/serine/threonine-rich
F:183-202/Domain: transmembrane #status predicted <TMN>
F:203-250/Domain: intracellular #status predicted <INT>
F:95,162/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.9%; Score 169.5; DB 1; Length 250;
Best Local Similarity 27.0%; Pred. No. 1.6e-05;
Matches 62; Conservative 29; Mismatches 94; Indels 45; Gaps 11;

QY 28 CDNCPGTF---CRKNPV---CKSCPST-PS-SIGQPNICRVACAGYFRFKTCSS 79
Db 40 CRKCPGTFVVKDQDRTAACDCPCIGTSPDYHTRPHCESCRHNSGLIRN-CTV 98
QY 80 THNACECIEGPHCLGPQCTRCCKDCRPGQBELTKGCKTCSLGTNDQNGTGVCRPWTNC 139
Db 99 TANABSCSKNQCRDQECTCEDPLNFA--LTRPSETSPQP-----PPTH- 144
QY 140 SLDGRSVLKTGTTKDVVCGPVVFSFSTTISVTPEGGPGHSLQVLTFLALTSALL 199
Db 145 -----LPHGTKEPSW-----PLHRQLPNTSVYQSRSHRPLCSDCIRIFVTSSMFLI 193
QY 200 ALIFITLLFSLVKIRKFFHIFKPKTKTGAQAEEDACSCRCPOBEEG 249
Db 194 FVLGAILFFHQR---RNHGNEDRQ-----AVREPCPYSCPREEG 232

RESULT 13
A46517
N:Alternate names: CD27L receptor; T cell activation antigen CD27
C:Species: Homo sapiens (man)
C:Date: 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
C:Accession: A46517; A46454
R:Loenen, W.A.; Gravestien, L.A.; Beumer, S.; Melief, C.J.; Hagemeijer, A.; Borst, J.
J. Immunol. 149, 3937-3943, 1992
A:Title: Genomic organization and chromosomal localization of the human CD27 gene.
A:Reference number: A46517; MUID:93094588; PMID:1334106
A:Accession: A46517
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-260 <LOE>
A:Note: sequence extracted from NCBI backbone (NCBIP:120386)
R:Canerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.
J. Immunol. 147, 3165-3169, 1991
A:Title: The T cell activation antigen CD27 is a member of the nerve growth factor/tumor
A:Reference number: A46454; MUID:92013149; PMID:1655907
A:Accession: A46454
A:Molecule type: mRNA
A:Residues: 1-58, 'A', 60-260 <CAM>
A:Cross-references: GB:M63928; NID:G180084; PIDN:AAA58411.1; PID:G180085
A:Note: sequence extracted from NCBI backbone (NCBIN:60285, NCBIP:60289)
C:Comment: A soluble CD27 found in serum and urine is formed by proteolysis.
C:Genetics:
A:Gene: GDB:CD27
A:Cross-references: GDB:132582; OMIM:186711
A:Map position: 12p13-12p13
A:Introns: 46/1; 90/1; 150/1; 180/1; 220/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; homodimer; phosphoprotein; receptor; surface anti
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-260/Product: CD27 antigen #status predicted <MAT>
F:27-63/Domain: extracellular #status predicted <EXT>
F:65-105/Domain: NGF receptor repeat homology <NG1>
F:121-188/Region: proline/serine/threonine-rich

F:192-211/Domain: transmembrane #status predicted <TMN>
F:212-260/Domain: intracellular #status predicted <INT>
F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.7%; Score 166.5; DB 1; Length 260;
Best Local Similarity 25.0%; Pred. No. 2.7e-05;
Matches 63; Conservative 25; Mismatches 85; Indels 79; Gaps 12;

QY 28 CDNCPGTF---CRKNPV---CKSCPSS-TFS-SIGQPNICRVACAGYFRFKTCSS 79
Db 40 COMCEPGETFLVKDQDRHTAQCDCPCIGVSPSPDHTRPHCESCRHNSGLLVN-CTI 98
QY 80 THNACECIEGPHCLGPQCTRCCKDCRPGQBELTKGCKTCSLGTNDQNGTGVCRPWTNC 139
Db 99 TANABSCSKNQCRDQECTCED-----PLNPN 126
QY 140 SLDGRSVLKTGTTKDVVCGPVVFSFSTTISVTPEGGPGHSLQVLTFLAL-- 193
Db 127 SUTARS-----SQALSPPHQPQTHLPYVSEMLEARTAGH-MQTLADFQLPA 171
QY 194 -----TSALLLALIFITLLFSLVKIRKFFHIFKPKTKTGAQAEEDAC 239
Db 172 RLSTHWPQORSLCSDDFIRILVIFSGMFLVTLGALFLH-ORRYKRNKGESPVPEAE 230
QY 240 SCR--CPQBEEG 249
Db 231 PCRYSCPREEG 242

RESULT 14
I48700
Gene: ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Bortwegh, A.J.; Claassen, E.; Noelle, R.J.; I
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell inte
A:Reference number: I48700; MUID:94044750; PMID:8228223
A:Accession: I48700
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CAA79772.1; PID:G312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A:Reference number: I48334; MUID:95255413; PMID:7737295
A:Accession: I48334
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14, 'G', 16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:G732818; PIDN:CAA59476.1; PID:G732819
C:Genetics:
A:Gene: ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
Query Match 11.1%; Score 158; DB 2; Length 272;
Best Local Similarity 23.8%; Pred. No. 0.00012;
Matches 57; Conservative 25; Mismatches 87; Indels 70; Gaps 10;

QY 8 VVIVLLVAGCEKVGAVONS-----CDNCPG-----TFC-RKYNPVCKSCPSTFSSI 55
Db 12 LLLALITLGVARRLNCVHTVPSHKKCRCPQGMVSRCDHTRDTLCHPCETGTFNEA 71
QY 56 GGQPNICRVACAGYFRFKTCSSTHNACECIEGPHCLGPQCTRCCKDCRPGQELTKQG 115
Db 72 VNYDTCKQCTQC-----NHRSGSELKQ--NCTPTQDTVCR--CRPGTQPPQDS 115
QY 116 -----CKTCSLGTNDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGP----- 160

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Matches 43; Conservative 12; Mismatches 54; Indels 47; Gaps 8;
Qy 28 CDNCQPETGPKY-----NFVCKSCPPTF--SSIGQQPNCNICR-VCAGYFRFKFGSST 80
Db      :|::||:
40 CASCHPGFYASRLCGPSNTVCSPCEDGTFTASTNHAFACVSCRGPCTGHLSSEQPDRT 99
Qy 81 HNAECCEIAGFCGLCPQTRCEKDCRPQEELTKQCCKTCSLGTENDONGTGVCERWINC- 139
Db      :|::||:
100 HDRVCMNSTGNVCL-----LKQGNGCRICAPQTACP 130

Qy 140 ---SLDGRSVLTGTT--EKDYVVGPPVVVSFPSPST 170
Db      :|::||:
131 AGYGVSCHT--RAGDTLCRK---CPPHTYSDSLST 161

RESULT 17
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N:Alternate names: NGF receptor
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0006; A60504
R:Large, T.H.; Weskamp, G.; Heller, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reichman, S.; Heuer, J.G.; Patemie-Nainie, S.; Wheeler, E.F.; Bothwell, M. Dev. Biol. 137, 287-304, 1990
A>Title: Structure and developmental expression of the nerve growth factor receptor in t: Neuron 2, 1123-1134, 1989
A:Reference number: JN0006; MID:90166579; PMID:2560385
A:Accession: JN0006
A:Molecule type: mRNA
A:Residues: 1-416 <LAR>
A:Experimental source: embryonic chick brain
R:Heuer, J.G.; Patemie-Nainie, S.; Wheeler, E.F.; Bothwell, M. Dev. Biol. 137, 287-304, 1990
A>Title: Structure and developmental expression of the chicken NGF receptor.
A:Reference number: A60504; MID:90152140; PMID:2154393
A:Accession: A60504
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 21-35,'Y','37'-172,'K','174-275','S','277'-395,'R','397'-416 <HEU>
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce...
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of t...
C:Comment: This protein is thought to form a high-affinity receptor when it associates w...
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t:...
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-416/Product: nerve growth factor receptor #status predicted <MAT>
F:21-239/Domain: extracellular #status predicted <EXT>
F:24-57/Domain: NGF receptor repeat homology <NG1>
F:59-100/Domain: NGF receptor repeat homology <NG2>
F:101-139/Domain: NGF receptor repeat homology <NG3>
F:141-181/Domain: NGF receptor repeat homology <NG4>
F:189-237/Region: serine/threonine-rich
F:240-261/Domain: transmembrane #status predicted <MEM>
F:262-416/Domain: intracellular #status predicted <INT>
F:52/Binding site: carbohydate (Asn) #status predicted

Query Match          9.8%; Score 139.5; DB 1; Length 416;
Best Local Similarity 25.7%; Pred. No. 0.0038;
Matches 53; Conservative 24; Mismatches 82; Indels 47; Gaps 12;

Qy 9 VIVILLVCCEKGAVQNSDNC-----QGTGCRKN-----PVCKSCPP 49
Db 5 VLPLDLLL----PAGTFWSGSKXCLTKMYTTSGECKACNLGEVGVQPGVNQTVCEPCLD 61

Qy 50 S-TFS-SIGQQPNCNICRVCAGYFRFKFCFSSTHNAECEIEGF-----HCLGPQCTR 100
Db 62 SVTYSDDTVSATPECKPKTCQCVGLHSMSAPCVESDDAVRCAYGFQDELSSGC--KECSI 119

Qy 101 CEK-----DCEPGGELLTKQCCKTCSLGTENDQ--NGTGVCBPWTNCSLDGRSVLKTGTE 153
Db 120 CENVGFLGMFFPCRDSDQTV--CBEECFGTSDFDEANFDVDPCLPCTICE-ENEVMVKECTAT 175

Qy 154 KDWC-----GGPVVSFPSSTTISVTPE 176
```

Db 176 SDAECRLHPRWTHTPSLAGSDSPE 201

RESULT 18
T28623
hypothetical protein G2R - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003
C:Accession: T28623
R:Masungu, R.P.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: EMBL:I22579; NID:G623595; PIDN:AAA60933.1; PID:9439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 9.7%; Score 138; DB 2; Length 348;
Best Local Similarity 22.6%; Pred. No. 0.0042;
Matches 59; Conservative 28; Mismatches 104; Indels 70; Gaps 11;

QY 28 CDNCPGTFCTC-----RKNYPVKSCPPSTFSSIGGQ-PNCNICR-VCAGYFRFKKFCST 80
Db 43 CLSCPPGTYASRLCDSKNTCTCPGSGTFTSRNNHLPACLSNCRNSNQVETRSNTT 102
QY 81 HNAECCEIEGFHCL---GPQCTRCCKDCRPGQELTKQG-----CKTCSLGTENDQ-N 128
Db 103 HNRICECPGYVCLLKGSSGCKACVSQTKGIGYGVSGHTSVGDIVICSPCGFGTYHTVS 162
QY 129 GTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVPSPSTTISVTPPEGGPGHSLQVLT 188
Db 163 SADKCEPVNNTFNVIDEITLYPVNDTSC-----TRTTTGLSES----- 203
QY 189 LFLALTSALLLAL-----IFITLLFSVLKWI-----RKFPPIFK----- 223
Db 204 ---ILTSELTITMHTDCNPFREYFVSVLNKVTATSGFTGENRYQNIISKVCTLNFEIKC 260
QY 224 ----QPFKKTGAQAEEDACS 240
Db 261 NNKGSSFKQLTKAKNDGWS 281

RESULT 19
D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:9456758; PIDN:CAA49137.1; PID:9457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46868
A:Accession: S46888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47540.1; PID:9516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakchchiev, L.S.

FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281; PMID:8384129
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics: G4R
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 9.7%; Score 138; DB 2; Length 349;
Best Local Similarity 22.6%; Pred. No. 0.0042;
Matches 59; Conservative 28; Mismatches 104; Indels 70; Gaps 11;

QY 28 CDNCPGTFCTC-----RKNYPVKSCPPSTFSSIGGQ-PNCNICR-VCAGYFRFKKFCST 80
Db 44 CLSCPPGTYASRLCDSKNTCTCPGSGTFTSRNNHLPACLSNCRNSNQVETRSNTT 103
QY 81 HNAECCEIEGFHCL---GPQCTRCCKDCRPGQELTKQG-----CKTCSLGTENDQ-N 128
Db 104 HNRICECPGYVCLLKGSSGCKACVSQTKGIGYGVSGHTSVGDIVICSPCGFGTYHTVS 163
QY 129 GTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVPSPSTTISVTPPEGGPGHSLQVLT 188
Db 164 SADKCEPVNNTFNVIDEITLYPVNDTSC-----TRTTTGLSES----- 204
QY 189 LFLALTSALLLAL-----IFITLLFSVLKWI-----RKFPPIFK----- 223
Db 205 ---ILTSELTITMHTDCNPFREYFVSVLNKVTATSGFTGENRYQNIISKVCTLNFEIKC 261
QY 224 ----QPFKKTGAQAEEDACS 240
Db 262 NNKGSSFKQLTKAKNDGWS 282

RESULT 20
S53868
laminin alpha-2 chain precursor - mouse
N:Alternate names: laminin M chain; merosin heavy chain
C:Species: Mus musculus (house mouse)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 10-Dec-1999
C:Accession: I49077; S50829; I48655; S31576; S53868
R:Bernier, S.M.; Utani, A.; Sugiyama, S.; Doi, T.; Pollistina, C.; Yamada, Y.
Matrix Biol. 14, 447-455, 1995
A:Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
A:Reference number: I49077; MUID:95316259; PMID:7795883
A:Accession: I49077
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3106 <RES>
A:Cross-references: EMBL:U12147; NID:969109; PIDN:AA52165.1; PID:9699110
R:Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
Nature Genet. 8, 297-302, 1994
A:Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (Lama2) ge
A:Reference number: S50829; MUID:95179178; PMID:7874173
A:Accession: S50829
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 64-281 <XUH>
A:Cross-references: GB:S75315; NID:9833929; PIDN:AA833573.1; PID:9833930
R:Chang, A.C.; Wadsworth, S.; Colligan, J.E.
J. Immunol. 151, 1789-1801, 1993
A:Title: Expression of merosin in the thymus and its interaction with thymocytes.
A:Reference number: I48655
A:Accession: I48655
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 2162-2204, 'D', 2206-2213, 'EY', 2216-2279 <RE2>

A:Cross-references: EMBL:X69869; NID:953055; PIDN:CAA9502.1; PID:953056
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C:Function:
 A:Description: interact with cells and with other basement membrane proteins to promote
 C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
 C:Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glyco
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
 F:283-337/Domain: laminin-type EGF-like homology <LE01>
 F:340-407/Domain: laminin-type EGF-like homology <LE02>
 F:410-462/Domain: laminin-type EGF-like homology <LE03>
 F:465-511/Domain: laminin-type EGF-like homology <LE04>
 F:514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
 F:720-750/Domain: laminin-type EGF-like homology <LE06>
 F:753-800/Domain: laminin-type EGF-like homology <LE07>
 F:803-858/Domain: laminin-type EGF-like homology <LE08>
 F:861-911/Domain: laminin-type EGF-like homology <LE09>
 F:914-960/Domain: laminin-type EGF-like homology <LE10>
 F:963-1007/Domain: laminin-type EGF-like homology <LE11>
 F:1010-1053/Domain: laminin-type EGF-like homology <LE12>
 F:1056-1099/Domain: laminin-type EGF-like homology <LE13>
 F:1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>
 F:1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>
 F:1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>
 F:1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>
 F:1416-1462/Domain: laminin-type EGF-like homology <LE18>
 F:1465-1520/Domain: laminin-type EGF-like homology <LE19>
 F:1523-1567/Domain: laminin-type EGF-like homology <LE20>
 F:2166-2327/Domain: laminin G repeat homology <LG1>
 F:2360-2520/Domain: laminin G repeat homology <LG2>
 F:2546-2709/Domain: laminin G repeat homology <LG3>
 F:2785-2933/Domain: laminin G repeat homology <LG4>
 F:2960-3106/Domain: laminin G repeat homology <LG5>

Query Match 9.7%; Score 138; DB 1; Length 3106;
 Best Local Similarity 26.7%; Pred. No. 0.024;
 Matches 54; Conservative 19; Mismatches 67; Indels 62; Gaps 13;

QY 23 AVQNSCDN-----CQGTCTCKYKVPVCKSPSTSSIGQENCNICRVACGYRFXK 75
 DB 870 SIPGCDLSLSSCLICKPDTGTR-----YCELCADGYFGDAVNTKPCPCRDINGSFSE 924
 QY 76 FOSTHNAECRC---IEGFHC-----LGPQCTRCED-----C 105
 DB 925 DC-HRTQTQCCRPNVQGHDECKPFTFGLQGRGLPCNCSFGSKSPDCASQCWC 983
 QY 106 PQGQLTKGCKTCLGTFNDONGTGVCRPTNCS-LDGRSVLTKGTEDKVVCGPPVVS 164
 DB 984 PQG---VAGKKCDRCAGHFNQEGGCTA---CDCSHLGNNDPKTG-----QCIC----- 1028
 QY 165 FSPSTTISVTPGPGG--GHSL 184
 DB 1029 -PPNTGKEKCECLPNTGHSI 1049

RESULT 21
 A35502
 Major surface-labeled trophozoite antigen precursor - Giardia lamblia
 C:Species: Giardia lamblia
 C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Sep-1997
 C:Accession: A35502
 R:Gilllin, F.D.; Hagblom, P.; Harwood, J.; Aley, S.B.; Reiner, D.S.; McCaffery, M.; So, M.
 Proc.Natl. Acad. Sci. U.S.A. 87, 4463-4467, 1990
 A:Title: Isolation and expression of the gene for a major surface protein of Giardia lam
 A:Reference number: A35502; MUID:90280395; PMID:2352929
 A:Accession: A35502
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-713 <GIL>
 A:Cross-references: GB:M33641; NID:g159131; PID:g159132
 C:Keywords: surface antigen; transmembrane protein

Query Match 9.5%; Score 135.5; DB 2; Length 713;

Best Local Similarity 25.6%; Pred. No. 0.011;
 Matches 58; Conservative 20; Mismatches 67; Indels 82; Gaps 15;

QY 15 LVGCE-----KVGAVQNSCD---NCO-PGTFCR-----KYNPVCKSCPSTFSIGGQ 58
 DB 312 LVTCSACTDGYKPSADKTTCEAVSNCKTPG--CKACSNCKENEVCCTDCDGVSTLPTSQ 369
 QY 59 PNC-NICRVACGYF-----RPFKFCSSHTNAECF-----CIEGFHCLGPGQCTRCCK 103
 DB 370 --CIDSCAKIGNYVYAGTEAGAKKCKECTAANKCTCDGQCOACNDGFKYKNGDACSPCH- 426
 QY 104 DCRPQQLTKGCKTCLGTFND-----BSCNCSAGTASDCTECPKALRYGDDGKGTGCGECCCTGTGAGACK-- 474
 DB 427 -----BSCNCSAGTASDCTECPKALRYGDDGKGTGCGECCCTGTGAGACK-- 474
 QY 137 TNCSL--DCRSVLK--TGTTB--KDVVCGPPVVSFSPSTTISVTPBG 177
 DB 475 -TCGLTIDGASCYSECATTEYPQNGVCAPKASRATPCNDSPIQNG 520

RESULT 22

GORUN

Nerve growth factor receptor precursor, low affinity (validated) - human
 N:Alternate names: NGF receptor
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
 C:Accession: A25218; A60204; S21689; I57638
 R:Johnson, D.; Lananhan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.;
 Cell 47, 545-554, 1986
 A:Title: Expression and structure of the human NGF receptor.
 A:Reference number: A25218; MUID:87051725; PMID:3022937
 A:Accession: A25218
 A:Molecule type: mRNA
 A:Residues: 1-427 <JOH>
 A:Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
 R:Marano, N.; Diezschold, B.; Earley Jr., J.J.; Schattman, G.; Thompson, S.; Grob, P.;
 J. Neurochem. 48, 225-232, 1987
 A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
 A:Reference number: A60204; MUID:87085574; PMID:3025363
 A:Accession: A60204
 A:Molecule type: Protein
 A:Residues: 29-31, 'T', '33-42, 'TT', '45-46, 'TX', '50-51, 'XX', '54-56 <MAR>
 A:Experimental source: melanoma cell line A875
 A:Note: This sequence has been corrected by a note added in proof to follow the nucleotic
 R:Visavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
 Arch. Biochem. Biophys. 294, 244-252, 1992
 A:Title: Structural domains of the extracellular domain of human nerve growth factor rece
 A:Reference number: S21689; MUID:92198017; PMID:1372492
 A:Accession: S21689
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 183-208 <VIS>
 R:Sehgal, A.; Patil, N.; Chao, M.
 Mol. Cell. Biol. 8, 3160-3167, 1988
 A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
 A:Reference number: I57638; MUID:89096903; PMID:2850481
 A:Accession: I57638
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-22 <RES>
 A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of t
 C:Comment: This protein is thought to form a high-affinity receptor when it associates w
 C:Comment: This receptor undergoes both N- and O-linked glycosylation.
 C:Genetics:
 A:Gene: GDB:NGFR
 A:Cross-references: GDB:I20234; OMIM:162010
 A:Map position: 17q21-17q22
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tr
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-427/Product: nerve growth factor receptor #status experimental <MAT>

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F:29-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>
F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          9.5%; Score 135; DB 1; Length 427;
Best Local Similarity 25.2%; Pred. No. 0.0083;
Matches 65; Conservative 26; Mismatches 97; Indels 70; Gaps 15;

QY 10 VIVLLVCEKGVAVQ-----NSCDNCQPGTF-----CRKYNPVKSCPPS-TFS 53
Db 15 LLLLLLVSLGGAKEACPTGLYTHSGECKACNLGEGVAQPCGANQTVCEPCLDSVTFS 74
QY 54 S-IGQPNICNCRVAGYFRFKFCSSTHNAECEIEGFHCLGPOCTCE--KDCRPGQE 110
Db 75 DVVSATEPKPCTECVGLQSMAPVEADDAVCRCAIYI-QDETTGRCEACRVCEAGSG 133
QY 111 LT-----KQG--CKTCSIGTFNDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEDKVVVC--- 158
Db 134 LVFSCQDKQNTVCEBCPDGTSDANHVDPCLPCTVCS-DTERQLRECTRWADAECBEIP 192
QY 159 -----GPPVVSFS--PSTTISVTPGEGG-----CHSLQVLT----- 188
Db 193 GRWITRSTPPGSDSTASTQ--EPEAPPEQDLIASTVAGVTVTVMGSSQPVVTRGTTD 249
QY 189 ----LFLALTGALLALI 202
Db 250 NLIPVYCSILAAVVGLV 267

RESULT 23
Integrin beta-5 chain - baboon
C:Species: Papio sp. (baboon)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
R:Shoji, M.; Hayzer, D.J.; Kim, T.M.; Runge, M.S.; Hanson, S.R.
Gene 133, 307-308, 1993
A:Title: Human and baboon integrin beta 5 subunit-encoding mRNAs have alternative polyad
A:Reference number: JC2005; MUID:94040831; PMID:8224922
A:Accession: JC2005
A:Molecule type: mRNA
A:Residues: 1-656 <SHO>
A>Note: The authors translated the codon AGA for residue 454 as Lys, CAA for residue 471
C:Comment: This protein is a predominant subunit for the vitronectin receptor in baboon
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology
C:Keywords: cell adhesion
F:320-370/Domain: laminin-type EGF-like homology <LEG>

Query Match          9.5%; Score 135; DB 2; Length 656;
Best Local Similarity 27.7%; Pred. No. 0.012;
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;

QY 27 SCDCNQ--PGTFCRKNPVCK----SCP--PSTFSSIGQPNICNCRVAGYFRFKFCS 78
Db 386 SCNQCSESEFGKIYGFCECDNFSCARNKGVLCSGHGECKCHAGIYDNCNC- 444
QY 79 STHNAECE-----CIEGFHCLGPQC-----TRCEK--DCRPGQELTKQGCKTCSL 121
Db 445 STDISTCRGRDQICSRGHCLCGCCQCTEPGAFGEMCEKCPCTC-PDACSTKRDCEVCEPL 503
QY 122 ---GTFNDQNGTGYCR----PWTNCSL--DGRSVLKTGTTEDKVVCGPPV---SPSPST 169
Db 504 LHSKPDNQICHSICRDEVITWDTIVKQDQEAFLCYFKTAKDCVMVMFTYVLPSPGSKNL 563
QY 170 TISVTPGEGGSHSLQVLTFLALTGALLALIFITLLFSVLKWI---RKPF 218
Db 564 TVLREPE---CGNTPNMTILLAVVGSILLVGLLAIWKLVIHTHIDREF 611

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RESULT 24
Integrin beta-5 chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 20-Aug-1999
C:Accession: A38308; A35775; S12534; S11708
R:McLean, J.W.; Vestal, D.J.; Chares, D.A.; Bodary, S.C.
J. Biol. Chem. 265, 17126-17131, 1990
A:Title: CDNA sequence of the human integrin beta-5 subunit.
A:Reference number: A38308; MUID:91009141; PMID:2211615
A:Accession: A38308
A:Molecule type: mRNA
A:Residues: 1-799 <MCL>
A:Cross-references: GB:J05633; NID:G186504; PIDN:AAAS9183.1; PID:G186505
A>Note: parts of this sequence, including the amino end of the mature protein, were confi
R:Suzuki, S.; Huang, Z.S.; Tanihara, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 5354-5358, 1990
A:Title: Cloning of an integrin beta subunit exhibiting high homology with integrin beta-
A:Reference number: A35775; MUID:90319111; PMID:2371275
A:Accession: A35775
A:Molecule type: mRNA
A:Residues: 1-192, A' 194-644, L' 646-789, 793-799 <SUZ>
A:Cross-references: GB:M35011; NID:G184524; PIDN:AAAS2707.1; PID:G306894
R:Ramawamy, H.; Hemler, M.E.
EMBO J. 9, 1561-1568, 1990
A:Title: Cloning, primary structure and properties of a novel human integrin beta subunit
A:Reference number: S12534; MUID:90228356; PMID:2328726
A:Accession: S12534
A:Molecule type: mRNA
A:Residues: 1-644, L' 646-799 <RAM>
A:Cross-references: EMBL:X53002; NID:G33952; PIDN:CAA37188.1; PID:G33953
C:Genetics:
A:Gene: GDB:ITGB5
A:Cross-references: GDB:128005; OMIM:147561
A:Map position: 17q11-17qter
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology
C:Keywords: cell adhesion; cytoskeleton; duplication; extracellular matrix; glycoprotein;
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-799/Product: Integrin beta-5 chain #status predicted <EXT>
F:25-719/Domain: extracellular #status predicted <EXT>
F:463-513/Domain: laminin-type EGF-like homology <LEG>
F:720-742/Domain: transmembrane #status predicted <TM>
F:743-799/Domain: intracellular #status predicted <INT>
F:347,460,477,505,552,586,654,705/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match          9.5%; Score 135; DB 2; Length 799;
Best Local Similarity 27.7%; Pred. No. 0.014;
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;

QY 27 SCDCNQ--PGTFCRKNPVCK----SCP--PSTFSSIGQPNICNCRVAGYFRFKFCS 78
Db 529 SCNQCSESEFGKIYGFCECDNFSCARNKGVLCSGHGECKCHAGIYDNCNC- 587
QY 79 STHNAECE-----CIEGFHCLGPQC-----TRCEK--DCRPGQELTKQGCKTCSL 121
Db 588 STDISTCRGRDQICSRGHCLCGCCQCTEPGAFGEMCEKCPCTC-PDACSTKRDCEVCEPL 646
QY 122 ---GTFNDQNGTGYCR----PWTNCSL--DGRSVLKTGTTEDKVVCGPPV---SPSPST 169
Db 647 LHSKPDNQICHSICRDEVITWDTIVKQDQEAFLCYFKTAKDCVMVMFTYVLPSPGSKNL 706
QY 170 TISVTPGEGGSHSLQVLTFLALTGALLALIFITLLFSVLKWI---RKPF 218
Db 707 TVLREPE---CGNTPNMTILLAVVGSILLVGLLAIWKLVIHTHIDREF 754

RESULT 25
A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)

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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A26431; PH1229
 R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
 Nature 325, 593-597, 1987
 A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
 A;Reference number: A26431; MUID:87115859; PMID:3027580
 A;Accession: A26431
 A;Molecule type: mRNA
 A;Residues: 1-425 <RAD>
 A;Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
 R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
 Gene 121, 247-254, 1992
 A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoic acid.
 A;Reference number: PH1229; MUID:93077038; PMID:1446821
 A;Accession: PH1229
 A;Molecule type: DNA
 A;Residues: 1-20 <MET>
 A;Cross-references: GB:X61269
 C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells, and on the cytosolic region of the extracellular domain may form part or all of a heterodimer.
 C;Comment: This protein is thought to form a high-affinity receptor when it associates with a heterodimer.
 C;Genetics:
 A;Introns: 20/3
 C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tyrosine kinase
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-425/Product: nerve growth factor receptor #status predicted <NAT>
 F;30-251/Domain: extracellular #status predicted <EXT>
 F;33-66/Domain: NGF receptor repeat homology <NG1>
 F;68-109/Domain: NGF receptor repeat homology <NG2>
 F;110-148/Domain: NGF receptor repeat homology <NG3>
 F;150-190/Domain: NGF receptor repeat homology <NG4>
 F;198-249/Region: serine/threonine-rich
 F;252-273/Domain: transmembrane #status predicted <MEM>
 F;274-425/Domain: intracellular #status predicted <INT>
 F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.3%; Score 133; DB 1; Length 425;
 Best Local Similarity 25.6%; Pred. No. 0.012;
 Matches 51; Conservative 20; Mismatches 88; Indels 40; Gaps 11;

QY 10 VIVLLVGCCKVAVQ-----NSDCNCPGTF-----CRKNPVCKSCPPS-TFS 53
 DB 16 LILLILVSSGSKETCTGLYHSGCCXACNLGEGVAGPCGANTVEPLDNTFS 75
 QY 54 S-IGGPNICIRVAGVFRFKFGCSSTHNAECIEBGF-----HCLGPGQTRCEK-- 103
 DB 76 DVVSATEPCCKTECLGLQSNAPVEADDAVCRCAVGYQDEETGHC--EACSVCEVGS 133
 QY 104 ---DCRPGQELTKGCKTCSLGTENDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVWC 158
 DB 134 GLVFSQCKQNTV---CCECEPGTYSDEANHVDPCLPTVCE-DTERQLRECTPWADAC 189
 QY 159 GPPVVSFSPSTTISVTPEG 177
 DB 190 EIPGRWIPRST---PPEG 205

Query Match 9.0%; Score 129; DB 2; Length 1797;
 Best Local Similarity 25.0%; Pred. No. 0.071;
 Matches 47; Conservative 13; Mismatches 46; Indels 82; Gaps 12;

QY 20 KYGAVQNSCDNCPQTFCKRYNPV-CKSC---PBSTFSSI----- 55
 DB 805 KPGVVGRRCDTCAPGY--GPGTCCQACQCSPPGALSSLCERTSGOCLCRTGAFGLRCD 862
 QY 56 -----GGQPNCTCRVAGVFRFKKCSSTHNAEC-----ECIEGFH---- 92
 DB 863 ACQRGQWGFPPSCRPC-VCNGH---ADEC-NHTGACLGCRDLTGGEHCERCIAGFHGDP 917
 QY 93 -CLGPGQ-----TRCKD-----CRPGQELTKGCKTCSLGTEND 126

C;Keywords: glycoprotein
 F;64-105/Domain: NGF receptor repeat homology <NG2>
 F;106-147/Domain: NGF receptor repeat homology <NG3>
 F;166-181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 130.5; DB 1; Length 326;
 Best Local Similarity 25.8%; Pred. No. 0.014;
 Matches 41; Conservative 22; Mismatches 49; Indels 47; Gaps 10;

QY 28 CDNCPGTFCKRY-----NPVCKSCPPSTF-SSIGQPNICR-VCAGYFRFKKCSST 80
 DB 40 CTSCEPGSYASRLGPGSDIVCSCKNETTASINHAPACVSCRGCTGHLSSQCDKT 99
 QY 81 HNARCECIEGPHCLGPGQTRCEKDCRPGQELTKGCKTCSLGTENDGTCVCRPTWC- 139
 DB 100 RDRVCDCSAGNYCL-----LKGQE-----GCR-----ICAPTKCP 130
 QY 140 ---SLDGRSVLKTGTTEKDVVCGP-PVVSFSPSTTISVT 174
 DB 131 AGYGVSGHT--RTG---DVLTKCPRYTSDAVSSTET 163

RESULT 27
 A5677
 laminin beta-2 chain precursor (version 1) - human
 C;Species: Homo sapiens (man)
 C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
 C;Accession: A5677
 R;Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Champlaud, M.F.;
 Genomics 24, 243-252, 1994
 A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal local
 A;Reference number: A5677; MUID:95213013; PMID:7698745
 A;Accession: A5677
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1797 <NEW>
 A;Cross-references: GB:X79683
 C;Genetics:
 A;Gene: GDB:LAMB2
 A;Cross-references: GDB:132363; OMIM:150325
 A;Map position: 3p21.3-3p21.2
 C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
 C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
 F;1-32/Domain: signal sequence #status predicted <SIG>
 F;33-1797/Product: laminin beta-2 chain #status predicted <NAT>
 F;283-344/Domain: laminin-type EGF-like homology <LE01>
 F;347-407/Domain: laminin-type EGF-like homology <LE02>
 F;410-467/Domain: laminin-type EGF-like homology <LE03>
 F;470-519/Domain: laminin-type EGF-like homology <LE04>
 F;522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>
 F;783-828/Domain: laminin-type EGF-like homology <LE06>
 F;831-874/Domain: laminin-type EGF-like homology <LE07>
 F;877-924/Domain: laminin-type EGF-like homology <LE08>
 F;927-982/Domain: laminin-type EGF-like homology <LE09>
 F;985-1034/Domain: laminin-type EGF-like homology <LE10>
 F;1037-1091/Domain: laminin-type EGF-like homology <LE11>
 F;1094-1139/Domain: laminin-type EGF-like homology <LE12>
 F;1142-1186/Domain: laminin-type EGF-like homology <LE13>

Db 918 LPYGAQCPCPCPEPGSGSRHATPSCHQDEYSQOIVCHCRAG--VTGLRCEACAPGQFGD 975
Qy 127 QNGTGVCR 134
Db 976 PSRPGACQ 983

RESULT 28

Tl0053
laminin alpha 5 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003
C:Accession: Tl0053
R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A:Reference number: Z16923
A:Accession: Tl0053
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3635 <MIN>
A:Cross-references: EMBL:U37501; NID:G2599231; PID:G2599232
C:Genetics:
A:Gene: Lama5
C:Keywords: basement membrane; cell binding; extracellular matrix
F:1988-1939/Domain: laminin-type EGF-like homology <LEG>
F:1942-1970/Domain: EGF homology <EGF>

Query Match 9.8%; Score 129; DB 2; Length 3635;
Best Local Similarity 27.2%; Pred. No. 0.12;
Matches 63; Conservative 14; Mismatches 65; Indels 90; Gaps 17;

Qy 27 SCNCCQGTGTCRKYNPVC--KSCPPSTFSSIGQPN-----CN-ICRVCAGYFRKFKCS 78
Db 1866 SCERCAGFP--GNPLVLGSSQPCDCSG-NGDPNWFSDCLPTGACRGLR----- 1915
Qy 79 STNABCE-CIEGFH--CLGPCTRCVKDQRP-----GQELTK- 113
Db 1916 HTTGPCHERCAPGYGNALLPNCNTRC--DCSPGCTETCDPSGRCLCKAGVTGQRCDRC 1973
Qy 114 -----GQCKTCSLG-----TFDQNGTGVCRPWTNCSLDGRSVLTKT-----GTT 152
Db 1974 LEGYFGEQCGCRPCACGPAKGSCHPQSQCHCQPGTT-----GPQCLCAPGYWGLP 2029
Qy 153 EK-----DVVCG-----PPVVSFSPSTTIS-----VTPEGGPGGSHL 184
Db 2030 EKGRCRQCPRGHCDPHTGCTCPPLSGERCDTCSQHQVFPVPGKPGGHGI 2081

RESULT 29

GORT1
tumor necrosis factor receptor 1 precursor - rat
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C:Accession: B36555
R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
A:Reference number: A36555; MUID:91090841; PMID:17029293
A:Accession: B36555
A:Molecule type: mRNA
A:Residues: 1-461 <HM>
A:Cross-references: GB:M63122; NID:G207361; PIDN:AAA42256.1; PID:G207362
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F:84-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>

F:168-204/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-461/Domain: intracellular #status predicted <INT>
F:54-151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.9%; Score 127; DB 1; Length 461;
Best Local Similarity 22.9%; Pred. No. 0.034;
Matches 58; Conservative 21; Mismatches 78; Indels 96; Gaps 11;

Qy 14 LLVGEKVGAVNSCDNCPGTFCKYNPV-----CKSCPSTFSSIGGPNCNICR--- 65
Db 69 LVSDCPSPQ-ETVCEVDKGIPTASQNHVRQCLSKTCRKMP-----QVEISPCKADM 121
Qy 66 --VC-AGYFRPKFCSTH-----NAECCEIEGFHCLGPOCTR 100
Db 122 DTVCGCKKNQFORVLSETHFQCVDCSPCFNGTVPCKEKNQTVNCNCHAGFFLSGNECTP 181
Qy 101 CEKDCRPGQELTKQCKTCSLGTFTNDQNGTGVCRPWTNCSLDGRSVLTKGTETKDVVCGP 160
Db 182 C-SHCKNQCEWK-----LCLP 197
Qy 161 PVVSFSPSTTISVTPEGGPGGSHLQVLFLLALISALLALIFITLFSVLKWKIRKFP 220
Db 198 PVA-----NVTNPQDSGTAVLLPLVIFLGL---CLLFFICISLLCRYPQWRPRVYSI 246
Qy 221 IFKQ--PEKKTG 231
Db 247 ICRSAPVKEVEG 259

RESULT 30

S18252
heparan sulfate proteoglycan - mouse
N:Alternate names: perlecan
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S18252; A31917; B31917; S66460
R:Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Has J. Biol. Chem. 263, 16379-16387, 1988
J. Biol. Chem. 266, 22939-22947, 1991
A:Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly adhesion molecule.
A:Reference number: S18252; MUID:92078153; PMID:1744087
A:Accession: S18252
A:Molecule type: mRNA
A:Residues: 1-3707 <NOO>
A:Cross-references: EMBL:M77174; NID:G200295; PIDN:AAA39911.1; PID:G200296
R:Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Has J. Biol. Chem. 263, 16379-16387, 1988
A:Title: Identification of cDNA clones encoding different domains of the basement membrar
A:Reference number: A32680; MUID:89034110; PMID:2972708
A:Accession: A31917
A:Molecule type: mRNA
A:Residues: 1870-2600 <NO3>
A:Cross-references: GB:J04055; NID:G200300; PIDN:AAA39912.1; PID:G200301
R:Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A:Title: Structural properties of recombinant domain III-3 of perlecan containing a globu
A:Reference number: S66460; MUID:95377282; PMID:7649154
A:Accession: S66460
A:Molecule type: protein
A:Residues: 1270-1274, 'X', 1276, 'X', 1278-1279 <SCH>
C:Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repe
C:Keywords: glycoprotein
F:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:764-811/Domain: laminin-type EGF-like homology <LEG>
F:1159-1206/Domain: laminin-type EGF-like homology <LEG7>


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Query Match      8.8%; Score 125.5; DB 1; Length 3084;
Best Local Similarity 26.8%; Pred. No. 0.2;
Matches 51; Conservative 16; Mismatches 58; Indels 65; Gaps 14;

QY 18 CEKVGAVONCDNCQP---GTFCKRY-----NPVCK--SCSPSTSSITGGGPNC--NIC 64
Db 813 CHLTDEEVVCDQCARFGYSGWCERCADGYGNPTVPGGTGVCPC-----NCSGND 863
QY 65 RVCAGYFRFKKFCSS-----THNAEC-CIEGFH---CLGPQCTRC-----102
Db 864 PLEAGH-----CDSVTGECIKLWNTDGAHCERCADGYGDAVTAKNCRACDCHENGSL 917
QY 103 -----KCRPRQGLTKQCKTCSLGTNDQNGTGVCRPWTNCSLDGRSVLKTGTT 152
Db 918 SGVCHLETGLCDCKP--HVTGQOCQDCLSGYGLDGTGLG-CVP-CNCSVEG-SVSDNCTE 972
QY 153 EKDWCQGPV 162
Db 973 EGQCHGCPGV 982

RESULT 32
T42629
tenascin-X - bovine
N/Alternate names: flexilin
C/Species: Bos primigenius taurus (cattle)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
R/Accession: T42629
R/RefSeq: F.; Exposito, J.Y.; Garrone, R.; Lethias, C.
J. Biol. Chem. 272, 22866-22874, 1997
A/Title: Characterization of the bovine tenascin-X.
A/Reference number: Z22180; MUID: 97426436; PMID: 9278449
A/Accession: T42629
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-4135 <EUE>
A/Cross-references: EMBL:Y11915; NID:G2462978; PIDN:CAA72671.1; PID:G2462979
C/Genetics:
A/Note: TN-X
C/Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C/Keywords: extracellular matrix; glycoprotein; heptad repeat

Query Match      8.8%; Score 125; DB 2; Length 4135;
Best Local Similarity 21.9%; Pred. No. 0.27;
Matches 56; Conservative 29; Mismatches 95; Indels 76; Gaps 13;

QY 18 CEKVGAVONS---CDNCQPGTFCKRYNPVCKSCPPSTSSITGGGPNC-----NITRV----- 66
Db 624 CHRGRCEGRCVDSGVTGSC-----ATKTCP-----ACRGRGRCVQGVCHVGYSG 674
QY 67 -----CAGYFRFKFCSSTHNAECIEGFHCLGPQCT--RCBKDCRPGQELT 112
Db 675 EDCGOEPPASACPGGCPRELCSA---GQCVCEGFR--GPDCAITCPGDCR-GRGEC 728
QY 113 KQCKTCSLGTNDQNG-----TGVCRPWNC--SLDGRSVLKTGTTTEK 154
Db 729 REGSCVODGAGDCGEEVAIEGRMHLEETVTEWTRAPGNVDVAYEIQFIPTTEG 788
QY 155 DWVCGPPVSPSTTISVTPEGGPGHSLQVL-----TLFLALTSALLL 199
Db 789 ---ASPPPTARVPSSASAYDQGLAPQEQVTVTRALRGTNWGPASKTITTMIDPQDL 845
QY 200 ALIFITLLFSVLKIR 215
Db 846 RWAVTPTTLELNWLR 861

RESULT 33
NMHVB1
laminin beta-1 chain precursor - human
N/Alternate names: laminin chain B1
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 19-Jan-2001
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C/Accession: S13547; A28483; A26994; S23566
R/Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.
J. Biol. Chem. 265, 15611-15616, 1990
A/Title: Structure of the human laminin B1 chain gene.
A/Reference number: S13547; MUID: 90368768; PMID: 1975589
A/Accession: S13547
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1786 <VUO>
A/Cross-references: GB:M61951; GB:J02778; NID:9186911; PIDN:AAA59486.1; PID:9186913
A/Note: The nucleotide sequence was submitted to Genbank, February 1991
R/Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, T.; Pihlajaniemi, T.; Saras
J. Biol. Chem. 262, 10454-10462, 1987
A/Title: Human laminin B1 chain. A multidomain protein with gene (LAMBI) locus in the q2?
A/Reference number: A28483; MUID: 87280097; PMID: 3611077
A/Accession: A28483
A/Molecule type: mRNA
A/Residues: 1-1786 <PIK>
A/Cross-references: GB:M61951; GB:J02778; NID:9186911; PIDN:AAA59486.1; PID:9186913
R/Jaye, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.
Am. J. Hum. Genet. 41, 605-615, 1987
A/Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localizati
A/Reference number: A26994; MUID: 88021029; PMID: 3661559
A/Accession: A26994
A/Molecule type: mRNA
A/Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>
R/Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P
A/Title: Genes for the human laminin B1 and B2 chains.
A/Reference number: S23566
A/Accession: S23566
A/Molecule type: DNA
A/Residues: 762-1786 <VU2>
A/Note: mRNA was also sequenced
C/Genetics:
A/Gene: GDB:LAMBI
A/Cross-references: GDB:119357; OMIM:150240
A/Map position: 7q31.1-7q31.3
A/Annotations: 13/1; 71/3; 117/1; 141/3; 204/3; 226/3; 293/3; 334/1; 397/1; 457/1; 494/3; 521
64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin <
C/Function:
A/Description: interact with cells and with other basement membrane proteins to promote <
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C/Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F/1-21/Domain: signal sequence #status predicted &ltSIG>
F/22-1786/Product: laminin beta-1 chain #status predicted &ltMAT>
F/22-270/Domain: VI &ltDOM6>
F/271-548/Domain: V &ltDOM5>
F/271-332/Domain: laminin-type EGF-like homology &ltLE01>
F/335-395/Domain: laminin-type EGF-like homology &ltLE02>
F/398-455/Domain: laminin-type EGF-like homology &ltLE03>
F/458-507/Domain: laminin-type EGF-like homology &ltLE04>
F/463-468/Region: cell adhesion #status predicted
F/510-540/Domain: laminin-type EGF-like homology #status atypical &ltLE05>
F/549-774/Domain: IV &ltDOM4>
F/662-668/Region: cell adhesion #status predicted
F/773-818/Domain: laminin-type EGF-like homology &ltLE06>
F/775-1178/Domain: III &ltDOM3>
F/821-864/Domain: laminin-type EGF-like homology &ltLE07>
F/867-914/Domain: laminin-type EGF-like homology &ltLE08>
F/917-973/Domain: laminin-type EGF-like homology &ltLE09>
F/923-927/Region: cell adhesion #status predicted
F/950-954/Region: cell adhesion #status predicted
F/976-1025/Domain: laminin-type EGF-like homology &ltLE10>
F/1028-1081/Domain: laminin-type EGF-like homology &ltLE11>
F/1084-1129/Domain: laminin-type EGF-like homology &ltLE12>
F/1132-1176/Domain: laminin-type EGF-like homology &ltLE13>
F/1179-1397/Domain: II &ltDOM2>
F/1179-1397/Region: heptad repeats
F/1398-1430/Domain: alpha &ltALP>
F/1431-1786/Domain: I &ltDOM1>
```

F:1431-1786/Region: heptad repeats
F:120-35/Disulfide bonds: #status predicted
F:130,356,519,677,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate
F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 8.7%; Score 124.5; DB 1; Length 1786;
Best Local Similarity 25.9%; Pred. No. 0.15;
Matches 45; Conservative 19; Mismatches 63; Indels 47; Gaps 13;

QY 1 MGNNVNVVVILLV-----GCEKGVAVNSCD-----NCQPGVFCRKNPVCKSC 47
DB 751 MTDVCRNIIPTISALLHQGLACEDPQGLSVCDPNGGQCQCRPNVGR-----TCNRC 806
QY 48 PSTFSSIGQPNMNCIRVACGYFRKFKCSSTHNAECIEGFH-----CLG-----P 96
DB 807 APGTGFG--GPSCKPCE--CHLQGSVNAFCNFV--TQCHCFQGVARQCDRLPGHWGFP 862
QY 97 QCTRC-----KDCRP--QELTKQ-----GCKTCLSTENDQ--NGTG--VCRP 135
DB 863 SCQPCQNGHADDCPVTGCLNCQDYTMGHNCERCLAGYDPIIGSDHCRP 916

RESULT 34
G02428
subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
C:Accession: G02428
R:Reudelhuber, T.L.
Submitted to the EMBL Data Library, February 1996
A:Reference number: H01242
A:Accession: G02428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-899 <REU>
A:Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C:Genetics:
A:Gene: PCS
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:148-386/Domain: subtilisin homology <SBT>

Query Match 8.7%; Score 124; DB 2; Length 899;
Best Local Similarity 22.2%; Pred. No. 0.096;
Matches 53; Conservative 21; Mismatches 61; Indels 104; Gaps 14;

QY 16 VGEKVGAVQ--NSC-----DNCQPGTF-----CRKNPVCKSCPSTFS 53
DB 629 VGCDGPGDHCNDCLHYVYKLNKNTICVSSCPGHYHDKRCKRKPNCESC-----FG 684
QY 54 SIGSQ-----PNC-----NCRVACGYFRFKFCSSTHNAEC 85
DB 685 SHGQCMSCVKGYFLNETNSCVTHCPDGSYQDTKNLCRKCS---ENCKTCTEFHNC-T 740
QY 86 ECIEGFHCLGPQCT-RCE-----KDCRPQELT-----KQCKTCSLGTG----- 124
DB 741 ECRDGLSLQGRSCVSCDGRYFNGQDQCPCHRFACATCAGAGADGCINCTEGYFMEGDCR 800
QY 125 -----NDQNGTGVCRP-----WTNC-SLDGRSVLKTGTTEKDVVC 158
DB 801 VQSCSISYFDFHSSSENGYKCKCDISCLTCNGPGFKNCTSCPSGYLLDLCMQMGAIC 859

RESULT 35
JC6148
subtilisin-like proprotein convertase (EC 3.4.21.-) homolog - human
N:Alternate names: PCA protease
C:Species: Homo sapiens (man)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: JC6148
R:Miranda, L.; Wolf, J.; Pichuanes, S.; Duke, R.; Franzusoff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A:Title: Isolation of the human PC6 gene encoding the putative host protease for HIV-1 g

A:Reference number: JC6148; MUID:96353880; PMID:8755538
A:Contents: CEM T-cell
A:Accession: JC6148
A:Molecule type: mRNA
A:Residues: 1-915 <MIR>
A:Cross-references: GB:U56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C:Comment: This protein functions as a soluble enzyme within the secretory pathway. It is
C:Genetics:
A:Gene: pc6A
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:164-402/Domain: subtilisin homology <SBT>

Query Match 8.7%; Score 124; DB 2; Length 915;
Best Local Similarity 22.2%; Pred. No. 0.097;
Matches 53; Conservative 21; Mismatches 61; Indels 104; Gaps 14;

QY 16 VGEKVGAVQ--NSC-----DNCQPGTF-----CRKNPVCKSCPSTFS 53
DB 645 VGCDGPGDHCNDCLHYVYKLNKNTICVSSCPGHYHDKRCKRKPNCESC-----FG 700
QY 54 SIGSQ-----PNC-----NCRVACGYFRFKFCSSTHNAEC 85
DB 701 SHGQCMSCVKGYFLNETNSCVTHCPDGSYQDTKNLCRKCS---ENCKTCTEFHNC-T 756
QY 86 ECIEGFHCLGPQCT-RCE-----KDCRPQELT-----KQCKTCSLGTG----- 124
DB 757 ECRDGLSLQGRSCVSCDGRYFNGQDQCPCHRFACATCAGAGADGCINCTEGYFMEGDCR 816
QY 125 -----NDQNGTGVCRP-----WTNC-SLDGRSVLKTGTTEKDVVC 158
DB 817 VQSCSISYFDFHSSSENGYKCKCDISCLTCNGPGFKNCTSCPSGYLLDLCMQMGAIC 875

RESULT 36
S14458
laminin alpha-1 chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 19-Jan-2001
C:Accession: S14458; S14563; A34961
R:Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
A:Title: Molecular cloning of the cDNA encoding human laminin A chain.
A:Reference number: S14458; MUID:91333420; PMID:1714537
A:Accession: S14458
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3075 <HAA>
R:Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A:Title: Primary structure of the human laminin A chain. Limited expression in human tis
A:Reference number: S14663; MUID:91264789; PMID:2049067
A:Accession: S14663
A:Molecule type: mRNA
A:Residues: 1-227, 'FE', 230-251, 'MLP', 255-418, 'E', 420-518, 'L', 520-1022, 'V', 1024-1074, 'V', 'J'
A:Cross-references: EMBL:X58531; NID:g34225; PIDN:CAA41418.1; PID:g34226
R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, J.
Lab. Invest. 60, 772-782, 1989
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A:Reference number: A34961; MUID:89280632; PMID:2733383
A:Accession: A34961
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'W', 2397-2745, 'L', 2747-3053, 'L', 3055-3072, 'PSP', <OLS>
A:Note: the authors translated the codon AGA for residue 2692 as Pro
C:Genetics:
A:Gene: GDB:LAMA1; LAMA
A:Cross-references: GDB:120135; OMIM:150320
A:Map position: 18p11.32-18p11.22
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bon
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-3075/Product: laminin alpha-1 chain #status predicted <MAT>

A>Note: the nucleotide sequence was submitted to GenBank, February 1991
 R: Pikkarainen, T.; Kallunki, T.; Tryggvason, K.
 J. Biol. Chem. 263, 6751-6758, 1988
 A: Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the
 A: Reference number: A28158; MUID: 88198245; PMID: 3360804
 A: Accession: A28158
 A: Molecule type: mRNA
 A: Residues: 1-211, 'I', 213-1609 <PIK>
 A: Cross-references: EMBL:J03202; NID: g186916; PID: AAAS9488.1; PID: g307107
 R: Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He
 Cytogenet. Cell Genet. 48, 137-141, 1988
 A: Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene to
 A: Reference number: S13549; MUID: 89169663; PMID: 3234037
 A: Accession: S13549
 A: Molecule type: mRNA
 A: Residues: 1393-1609 <FUK>
 A: Cross-references: EMBL: M27654; NID: g186923; PID: AAAS9489.1; PID: g186924
 R: Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
 Lab. Invest. 60, 772-782, 1989
 A: Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
 A: Reference number: A34961; MUID: 89280632; PMID: 2733383
 A: Accession: B34961
 A: Molecule type: mRNA
 A: Residues: 868-1551, 'N', 1553-1609 <OLS>
 R: Santos, C.L.S.; Sabbaga, J.; Brentani, R.
 DNA Seq. 1, 275-277, 1991
 A: Title: Differences in human laminin B2 sequences.
 A: Reference number: S14664; MUID: 92216129; PMID: 1806043
 A: Accession: S14664
 A: Molecule type: mRNA
 A: Residues: 1282-1609 <SAN>
 R: Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.
 in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P
 A: Title: Genes for the human laminin B1 and B2 chains.
 A: Reference number: S23566
 A: Accession: S23567
 A: Molecule type: DNA
 A: Residues: 801-1481, 'R', 1483-1609 <VUO>
 A: Note: mRNA was also sequenced
 C: Genetics:
 A: Gene: GDB: LAMC1; LAMB2
 A: Cross-references: GDB: 120136; OMIM: 150290
 A: Map position: 1q31-1q31
 A: Introns: 140/1; 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1;
 3; 1525/1
 C: Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C: Function:
 A: Description: interact with cells and with other basement membrane proteins to promote
 C: Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
 C: Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
 F: 1-33/Domain: signal sequence #status predicted <SIG>
 F: 34-1609/Product: laminin gamma-1 chain #status predicted <MAT>
 F: 34-285/Domain: VI <DOM6>
 F: 286-304/Domain: V <DOM5>
 F: 286-339/Domain: laminin-type EGF-like homology <LE01>
 F: 342-395/Domain: laminin-type EGF-like homology <LE03>
 F: 398-442/Domain: laminin-type EGF-like homology <LE04>
 F: 445-492/Domain: laminin-type EGF-like homology <LE04>
 F: 495-504/Domain: laminin-type EGF-like homology #status atypical <LE05>
 F: 505-689/Domain: IV <DOM4>
 F: 690-1034/Domain: III <DOM3>
 F: 690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>
 F: 724-770/Domain: laminin-type EGF-like homology <LE07>
 F: 773-825/Domain: laminin-type EGF-like homology <LE08>
 F: 828-881/Domain: laminin-type EGF-like homology <LE09>
 F: 884-932/Domain: laminin-type EGF-like homology <LE10>
 F: 935-980/Domain: laminin-type EGF-like homology <LE11>
 F: 983-1028/Domain: laminin-type EGF-like homology <LE12>
 F: 1035-1609/Domain: II/I <DOM1>
 F: 1035-1609/Region: heptad repeats
 F: 40-50/Disulfide bonds: #status predicted
 F: 60,134,576,650,1022,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carbonyl

F: 1031,1034,1600/Disulfide bonds: interchain #status predicted
 Query Match 8.6%; Score 122.5; DB 1; Length 1609;
 Best Local Similarity 24.2%; Pred. No. 0.2; Mismatches 56; Indels 91; Gaps 17;
 Matches 54; Conservative 22
 QY 18 CEKVG-----AVQNSCDNCP-----GTFC-----RKYNPVCKSCPSPSTSSIGGQPNM 62
 DB 751 CEKSDGYGUSTAGTSSDCQPCPGSSCAVVPKTKVAVCTNCPGTGTTGK-----RCE 805
 QY 63 ICRVCAGYF-----RPFKFCSTHN-----AEC-ECI-----EGPHC-- 93
 DB 806 LCD--DGYFGDPLGRNGPVLRLCLQCQSDNIDNNAVGNRLTGECLKCIYNTAGFYCDR 863
 QY 94 -----LGP-----OCTRC-----EKDCRP--QQ-----ELTKQGCKTCSLGT 123
 DB 864 CKDFFGNLAPNADKCAKCNPNYTMQKQSSCNVTVGCECLPHVTGDCGACDPPG 923
 QY 124 FNDQNGTGVCRPTWNC-----SLDGRSVLTKTGTTEKDVVCGPPV 162
 DB 924 YNLQSGQGCER--CDCHALGSTNGQCDIRTTGQCE-----CQPGI 960
 RESULT 39
 Hypothetical protein F55H12.3 - Caenorhabditis elegans
 C: Species: Caenorhabditis elegans
 C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
 C: Accession: T22759
 R: Dobson, R.
 Submitted to the EMBL Data Library, October 1996
 A: Reference number: Z19610
 A: Accession: T22759
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-2824 <WIL>
 A: Cross-references: EMBL: Z81091; PID: CAB03143.1; GSPDB: GN00019; CESP: F55H12.3
 A: Experimental source: clone F55H12
 C: Genetics:
 A: Gene: CESP: F55H12.3
 A: Map position: 1
 A: Introns: 87/1; 98/1; 126/2; 201/3; 343/3; 406/1; 576/3; 656/1; 825/3; 869/1; 909/1; 963/1;
 7/1; 1755/2; 1800/3; 1896/1; 2003/3; 2035/3; 2082/3; 2113/1; 2144/1; 2200/2; 2275/2
 C: Superfamily: LDL receptor ligand-binding repeat homology
 F: 243-279/Domain: LDL receptor ligand-binding repeat homology <LDL>
 Query Match 8.6%; Score 122.5; DB 2; Length 2824;
 Best Local Similarity 23.6%; Pred. No. 0.31;
 Matches 59; Conservative 31; Mismatches 113; Indels 47; Gaps 13;
 QY 22 GAVQNS-C-DNCQPGTFCRKYNPVCKSCPSPSTSSIGGQPNMTCRVCAGYFRFKFCSS 79
 DB 2470 GAVDESQCYVNCPIQFESK--GLNCPCEGTGTTGLRKC-----ICCG-----FDLS 2517
 QY 80 THNAEC-ECIEG-----FHLGPCTCEKDCRPGQELT-KQGKTCSL 121
 DB 2518 TFGGPCIQCPRLTTSQASTSINSCDINCIDAN-TMINKNVTVPSTPYSEICACEQ 2576
 QY 122 GFENDQNGTGVCRPTWNCSDGRSVLKT-GTTEKDV-----CGPPVVSPTSSTISVT 174
 DB 2577 GTFQVNSDSDCIPCDISENATSPVTCQSCSDAIPTAGCNCLQNGKSSMITRNL 2636
 QY 175 PEGGPGHSLQVLTFLALTSAALLALIFITLLF---SVLKWIRK-----KPHIFKQPFK 227
 DB 2637 PEVTPVPGNSAIKIVLGVFGVGLLIIVLVCFKQIIAIFRKTDTSDNQHVALSHWD 2696
 QY 228 KITGAARQED 237
 DB 2697 NATNRNEEN 2706
 RESULT 40
 T23433

hypothetical protein K08C7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T23433
R:Berks, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19740
A:Accession: T23433
A:Status: preliminary; translated from GB/EMBL/DDAJ
A:Molecule type: DNA
A:Residues: 1-3672 <WIL>
A:Cross-references: EMBL:Z70286; PIR:CAA94293.1; GSPDB:GN00022; CESP:K08C7.3
A:Experimental source: clone K08C7
C:Genetics:
A:Gene: CESP:K08C7.3
A:Map position: 4
A:Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like H

Query Match 8.6%; Score 122.5; DB 2; Length 3672;
Best Local Similarity 28.5%; Pred. No. 0.38;
Matches 49; Conservative 11; Mismatches 49; Indels 63; Gaps 12;

QY 13 LLLVGEKVGAVQNSDNCQPCTF-----CRKNPV-CKSCEPSTFSIG 56
||| : | : | : | : | : | : | : | : | : | : | :
Ddb 1902 LLQCNC-KPGYTGDRCDCASGFFGHPIGS CSPCCNGNNLTDSRCHPNSGCYL 1960
||| : | : | : | : | : | : | : | : | : | : | :
QY 57 GQPCNCL-ICRVAGYFR----FKFCSSTHNAECEIE---GFHCL----G 95
||| : | : | : | : | : | : | : | : | : | : | :
Db 1961 CEQNTDGRHCESCAAFWGDAVTAKNCSS-----CECSQGSGQYCDKSGCGECKINVEG 2015
||| : | : | : | : | : | : | : | : | : | : | :
QY 96 PQCTCEKD-----CRPQEELTKGGCKTCSLGT--FNQ-----NGTGVCRP 135
||| : | : | : | : | : | : | : | : | : | : | :
Db 2016 DSCDRCKPDHWGFSKC-----QGCGCHGTAFAFTQCNVENGOCTCRP 2059
||| : | : | : | : | : | : | : | : | : | : | :

Search completed: May 5, 2004, 14:41:21
Job time : 32.6849 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:56 ; Search time 20.1644 Seconds
(without alignments)
661.065 Million cell updates/sec

Title: US-10-067-122B-2

Perfect score: 1428

Sequence: 1 MGNCCYVNVVILLVGCEK.....DACSCRCQBEEGGGGYEL 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1428	100.0	256	1	TNR9_MOUSE
2	795	55.7	255	1	Q07011 homo sapien
3	237	16.6	415	1	TNR3_MOUSE
4	215	15.1	625	1	TR11_MOUSE
5	208.5	14.6	277	1	TNR5_HUMAN
6	203.5	14.4	616	1	TR11_MOUSE
7	203.5	14.3	228	1	TR18_MOUSE
8	202.5	14.2	277	1	TNR4_HUMAN
9	202	14.1	435	1	TNR3_HUMAN
10	197	13.8	241	1	TR18_MOUSE
11	197	13.8	461	1	TR18_HUMAN
12	188	13.2	401	1	TR18_MOUSE
13	186.5	13.1	289	1	TNR5_MOUSE
14	185	13.0	300	1	TR6B_MOUSE
15	185	13.0	474	1	TR21_MOUSE
16	180.5	12.6	655	1	TR1B_MOUSE
17	179	12.5	401	1	TR1B_MOUSE
18	177	12.4	401	1	TR1B_MOUSE
19	176.5	12.4	283	1	TR1A_HUMAN
20	170.5	11.9	271	1	TNR4_MOUSE
21	170	11.9	655	1	TR21_MOUSE
22	169.5	11.9	250	1	TNR7_MOUSE
23	167	11.7	269	1	TNR5_MOUSE
24	166.5	11.7	260	1	TNR7_HUMAN
25	158	11.1	272	1	TNR4_MOUSE
26	141.5	9.9	3695	1	LMA5_HUMAN
27	140.5	9.8	325	1	TR2_SFVKA
28	139.5	9.8	415	1	TR16_CHICK
29	138	9.7	349	1	CRMB_VSV
30	138	9.7	3106	1	LMA2_MOUSE
31	135.5	9.5	713	1	TS44_GIALA
32	135.5	9.5	3110	1	LMA2_HUMAN
33	135	9.5	427	1	TR16_HUMAN

ALIGNMENTS

RESULT 1

TNR9_MOUSE	ID	TNR9_MOUSE	STANDARD;	PRT;	256 AA.
AC	P20334;				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	01-FEB-1991 (Rel. 17, Last annotation update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB				
DE	ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).				
GN	TNFRSF9 OR ILA OR IY63 OR CD137 OR CD157.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89184547; PubMed=2784565;				
RA	Kwon B.S., Weissman S.M.;				
RT	"CDNA sequences of two inducible T-cell genes.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BAUS/C;				
RX	MEDLINE=94179605; PubMed=8133039;				
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;				
RT	"Genomic organization and chromosomal localization of the T-cell				
RT	antigen 4-1BB.";				
RL	J. Immunol. 152:2256-2262(1994).				
RN	[3]				
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.				
RX	MEDLINE=93139510; PubMed=7678621;				
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.;				
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and				
RT	function.";				
RL	J. Immunol. 150:771-781(1993).				
CC	-!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T				
CC	cell activation.				
CC	-!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.				
CC	ASSOCIATES WITH P56-LCK. Interacts with TRAF1, TRAF2 AND TRAF3 (By				
CC	similarity).				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.				
CC	-!- INDUCTION: Optimal by PMA and ionomycin.				
CC	-!- SIMILARITY: Contains 4 TNFR-Cys repeats.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; J04492; AAA40167.1; -				
CC	EMBL; U02567; AAA93113.1; -				
DR					
DR					

34	135	9.5	655	1	ITB5_PAPCY	Q07441 papio cynoc
35	134.5	9.4	386	1	T10D_HUMAN	Q9ubn6 homo sapien
36	134	9.4	799	1	ITB5_HUMAN	P18084 homo sapien
37	133.5	9.3	351	1	CRMB_COMPEX	O73559 cowpox viru
38	133	9.3	332	1	TNR6_PIG	O77736 sus scrofa
39	133	9.3	425	1	TR16_RAT	P07174 rattus norv
40	132.5	9.3	349	1	CRMB_CAMPS	Q8uya7 camelpox vi
41	131	9.2	417	1	TR16_MOUSE	Q9z0w1 mus musculu
42	130.5	9.1	326	1	VT2_MYXVL	P29825 myxoma viru
43	130	9.1	176	1	TR23_MOUSE	Q9er63 mus musculu
44	130	9.1	498	1	TNR8_MOUSE	Q60846 mus musculu
45	129	9.0	3718	1	LMA5_MOUSE	Q61001 mus musculu

DR PIR; B32393; B32393.
 DR FDB; 26-SEP-01.
 DR MGD; MGI:1101059; Tnfrsf9.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 1.
 DR SMART; SM00208; TNFR_2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00500; TNFR_NGFR_2; FALSE_NEG.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 256
 FT DOMAIN 25 256
 FT TRANSMEM 25 187
 FT DOMAIN 188 208
 FT DOMAIN 209 256
 FT REPEAT 17 45
 FT REPEAT 46 85
 FT REPEAT 86 117
 FT REPEAT 118 159
 FT REPEAT 159 187
 FT DISULFID 28 37
 FT DISULFID 31 44
 FT DISULFID 47 61
 FT DISULFID 64 77
 FT DISULFID 67 85
 FT DISULFID 87 93
 FT DISULFID 98 105
 FT DISULFID 101 116
 FT DISULFID 119 133
 FT DISULFID 139 158
 FT CARBOHYD 128 138
 FT CARSCHYD 138 138
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;
 Query Match 100.08; Score 1428; DB 1; Length 256;
 Best Local Similarity 100.08; Pred. No. 2e-110;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNNYNNVWVLLVGVCKVGVQNSCDNCPQGTFCRKNPVCKSCPPSTFSSIGQPN 60
 Db 1 MGNNYNNVWVLLVGVCKVGVQNSCDNCPQGTFCRKNPVCKSCPPSTFSSIGQPN 60
 QY 61 CNICRVAGYFRFKFCSSTHNAECIEGHCLGPQCTRCCKDCRPGQBLTKQGCKTCS 120
 Db 61 CNICRVAGYFRFKFCSSTHNAECIEGHCLGPQCTRCCKDCRPGQBLTKQGCKTCS 120
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVGVCPVVSFSPSTTISVTPGGPG 180
 Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVGVCPVVSFSPSTTISVTPGGPG 180
 QY 181 GHSQVLTFLFALTSALLALIFITLFSVLKWKIRKFFHFKQPFKKTGAAQEDACS 240
 Db 181 GHSQVLTFLFALTSALLALIFITLFSVLKWKIRKFFHFKQPFKKTGAAQEDACS 240
 QY 241 CRCPQEEGGGGYEL 256
 Db 241 CRCPQEEGGGGYEL 256
 RESULT 2
 ID TNR9 HUMAN STANDARD; PRT; 255 AA.
 AC Q07011;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) ("T-cell antigen 4-1BB homolog) (T-cell antigen ILA) (CD137 antigen).
 DE (CD137 antigen).
 GN TNFRSF9 OR ILA OR CD137.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 EX MEDLINE=94374434; PubMed=808337;
 RA Aderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Rous E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
 RA "Molecular and biological characterization of human 4-1BB and its ligand";
 RT Eur. J. Immunol. 24:2219-2227(1994).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 EX MEDLINE=94085794; PubMed=8262389;
 RA Schwarz H., Tuckwell J., Lotz M.;
 RA "A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor family";
 RT Gene 134:295-298(1993).
 RN [3]
 RP REVISION TO 107.
 RA Schwarz H.;
 RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 EX MEDLINE=95347766; PubMed=7622190;
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;
 RA "Characterization of human homologue of 4-1BB and its ligand";
 RT Immunol. Lett. 45:67-73(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Pearce A.;
 RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 EX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley M., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
 RX MEDLINE=98078711; PubMed=9418902;
 RA Arch R.H., Thompson C.B.;
 RT "4-1BB and Oxa40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB";
 RL Mol. Cell. Biol. 18:558-565(1998).
 RN [8]
 RP INTERACTION WITH TRAF1 AND TRAF2.
 RX MEDLINE=98270914; PubMed=9607925;
 RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A., Goldstein M.D., Bangia N., DeBenedetto M.A., Mak T.W., Choi Y., Watts T.H.;
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by

RT	4-1BB ligand";
RL	J. Exp. Med. 187:1849-1862 (1998).
RN	[9]
RP	INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
RX	MEDLINE=2166267; PubMed=11804328;
RY	Jang I.-K., Lee S.-H., Kim H.-H., Hall J.M., Kim J.-D., Kwon B.S.;
SA	"A novel leucine-rich repeat protein (LRR-1): potential involvement in
SB	4-1BB-mediated signal transduction.";
SC	Mol. Cells 12:304-312 (2001).
SD	- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
SE	cell activation.
SF	- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with
SG	LRR-repeat protein 1/LRR-1.
SH	- SUBCELLULAR LOCATION: Type I membrane protein.
SI	- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
SJ	- SIMILARITY: Contains 4 TNFR-Cys repeats.
SK	- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
SL	WWW='http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm'.
SM	-----
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ST	entities requires a license agreement (See http://www.isb-sib.ch/announce/
SV	or send an email to license@isb-sib.ch).
SW	-----
SX	EMBL; U03397; AAA53133.1; --
SY	ENBL; LI2964; AAG62478.2; --
SZ	ENBL; AL009183; CAB57398.1; --
T0	ENBL; BC006196; AAH06196.1; --
T1	ENBL; I38426; I38426.
T2	Pfam; PF00020; TNFR_c6; 2.
T3	SMART; SM00208; TNFR_2.
T4	DR PROSITE; PS00652; TNFR NGFR 1; 1.
T5	DR PROSITE; PS00050; TNFR NGFR 2; 1.
T6	KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
T7	POTENTIAL.
T8	FT SIGNAL 1 17
T9	FT CHAIN 18 255
T10	DOMAIN 18 186
T11	EXTRACELLULAR (POTENTIAL).
T12	TRANSMEM 187 213
T13	DOMAIN 214 255
T14	CYTOPLASMIC (POTENTIAL).
T15	TNFR-CYS 1.
T16	TNFR-CYS 2.
T17	TNFR-CYS 3.
T18	TNFR-CYS 4.
T19	INTERACTS WITH LRR-1.
T20	BY SIMILARITY.
T21	BY SIMILARITY.
T22	BY SIMILARITY.
T23	BY SIMILARITY.
T24	BY SIMILARITY.
T25	BY SIMILARITY.
T26	BY SIMILARITY.
T27	BY SIMILARITY.
T28	BY SIMILARITY.
T29	N-LINKED (GLCNAC...) (POTENTIAL).
T30	N-LINKED (GLCNAC...) (POTENTIAL).
T31	FT CARBOHYD 138 138
T32	FT CARBOHYD 149 149
T33	SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;
T34	Query Match 55.7%; Score 795; DB 1; Length 255;
T35	Best Local Similarity 58.4%; Pred. No. 2e-58;
T36	Matches 149; Conservative 67; Mismatches 8; Gaps 6;

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EMBL; U29173; AAB68964.1; -
EMBL; L38423; AAB00846.1; -
EMBL; U30798; AAB81334.1; -
HSSP; O14763; IDOG.
DR MGD; MGI:104875; Ltbl.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR_3
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS0050; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 24 244
FT DOMAIN 245 415
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 298326A566AEF661 CRC64;

Query Match 16.6%; Score 237; DB 1; Length 415;
Best Local Similarity 27.0%; Pred. No. 2.2e-12;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;
QY 28 CDNCQPGTF-----CRKYNPVCKSPSTFSSIGGQ-PNCNICRVCAGYFRFKF--CSS 79
Db CSRCPPGFEFVAVCSRSQDTVCKTPHNSYNEHWNHLSLQCLPCDVLVGFVEVAPCTS 118
QY 80 THNAECIEGPHC--LGPQCTREKD-----CRPGQL-----TKQCKTCSLGTF- 124
Db DRKAECCQPMGSCVYLDNECHVEERLVCQPGTEAEVTDEIMDTDVNVCVCKPGHFQ 178
QY 125 NDQNGTGVCRWTNCSLDGRSLVLTGTEKDVCGPPVWSFSTTISVTPGPGGHS 184
Db NTSSPRACQPHTEKCTQGLVEAPGYSYDTCKNP-----PFG----- 219
QY 185 QVTLFLALTSALLALIFLTLFSLVKWIR-----KKFPHFKQPKTKTGAQEDAC 239
Db 220 --AMLLAILLSLVFLFLFTVL--ACAMWRHPSLCKRKLTLKR-----HPEGEESP 268
QY 240 SCRCPOEE 247
Db 269 PCAPRAD 276

RESULT 4
ID TR11 MOUSE STANDARD; PRT; 625 AA.
AC O35305; OSVCT7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor

DE (Receptor activator of NF-KB) (Osteoclast differentiation factor
GN receptor) (ODFR).
CN TNFRSF11A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
EX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tomesko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
RL Nature 390:175-179 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
EX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP FUNCTION.
EX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400 (1998).
CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for
RANKL-mediated osteoclastogenesis. Involved in the regulation of
interactions between T-cells and dendritic cells.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL; AF019046; AAB6810.1; -
DR EMBL; BC019185; AAB19185.1; -
DR HSSP; P25942; 1CDF.
DR MGD; MGI:1314891; Tnfrsf11a.
GO; GO:0007275; P:development; IMP.

DR GO: GO:0007515; P: lymph gland development; IMP.
DR GO: GO:0001503; P: ossification; IMP.
DR InterPro: IPR001368; TNFR c6.
DR Pfam: PF00020; TNFR c6; 3.
DR SMART: SMO0208; TNFR; 4.
DR PROSITE: PS00652; TNFR NGFR 1; 1.
DR PROSITE: PS00500; TNFR NGFR 2; 1.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 625
FT DOMAIN 31 625 TUMOR NECROSIS FACTOR RECEPTOR
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT TNFR-CYS 4.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLNAC. .) (POTENTIAL).
FT N-LINKED (GLNAC. .) (POTENTIAL).
FT R -> K (IN REF. 2).
SQ SEQUENCE 625 AA; 66621 MW; P8C1872B99511D8E CRC64;
Query Match 15.1%; Score 215; DB 1; Length 625;
Best Local Similarity 28.6%; Pred. No. 2.1e-10;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;
QY 28 CDNCQPTG-CRKNP-----VKSCPPSTP-SGIGQPNICRCVAGYFRFKKFCSSSTH 81
DB 48 CSRCEPKYLSSKTPSDSVCLPCGDEYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107
QY 82 NA-EECEIEGFH-----CLGPQTRCEKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127
DB 108 TAPRCACAGYHWNDC---ECRRNTECAPGAGHPQLNKNQVCTPCLLGFSDVDF 164
QY 128 NGTGVCRPWNCSLDGRSVLTKGTTEKDVVCGPPVWSFSPSTTISVTP-EGGPGGHSLOV 186
DB 165 SSTDKCKPWNCTLLGKLEAHQGTESDVVC-----SSSMTLRPPKRAQAYLPSLIV 217
QY 187 LTFLAITSALLIALIF-----ITLFSVLKWKRPKPHFKQFFKTKTGAQAEEDA 239
DB 218 LLLFISV--VVVAIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSRCRCPOEERG 250
DB 255 CSSLSGNKRESSG 266
RESULT 5
ID TNRS HUMAN STANDARD; PRT; 277 AA.
AC P25942; Q9BYU0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=89356608; PubMed=2475341;
RX Stamenkovic I., Clark E.A., Seed B.;

"A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas";
EMBO J. 8:1403-1410(1989).
[2]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehaeslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., McElay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rameay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A.S., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20";
Nature 414:865-871(2001).
[3]
RP SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=21117110; PubMed=11172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through alternative splicing";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
[4]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX TISSUE=Ovary;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling";
Science 267:1494-1498(1995).
[6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216;

RA Sato T., Izie S., Reed J.C.;
RT "A novel member of the TRAF family of putative signal transducing
RL proteins binds to the cytosolic domain of CD40.";
RN FEBS Lett. 358:113-118(1998).
RP INTERACTION WITH TRAF1; TRAF2; TRAF3 AND TRAF5.
RX MEDLINE=98384149; PubMed=9718306;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
RA Kehy M.R.;
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
RT interactions: regulation of CD40 signaling through multiple TRAF
RT binding sites and TRAF hetero-oligomerization.";
RL Biochemistry 37:11836-11845(1998).
RN [8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
RN [9]
RP INTERACTION WITH TRAF6.
RX MEDLINE=98095703; PubMed=9432981;
RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,
RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.;
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
RT extracellular signal-regulated kinase (ERK) activity in CD40
RT signaling along a ras-independent pathway.";
RL J. Exp. Med. 187:237-244(1998).
RN [10]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [11]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Heu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=20442386; PubMed=10984535;
RA Ni C.Z., Welsh K., Leo E., Chou C.K., Wu H., Reed J.C., Ely K.R.;
RT "Molecular basis for CD40 signaling mediated by TRAF3.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=22000222; PubMed=12005438;
RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
RA Satterthwaite A.C., Cheng G., Ely K.R.;
RT "Downstream regulator TRAF3 binds to the CD40 recognition site on
RT TRAF3.";
RL Structure 10:403-411(2002).
RN [14]
RP VARIANT HIGM3 ARG-83.
RX MEDLINE=21532985; PubMed=11675497;
RA Ferrari S., Gilliani S., Insalaco A., Al-Chonaib A., Soresina A.R.,
RA Loubser M., Avanzini M.A., Marconi M., Badolato B., Ugazio A.G.,
RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
RA Flebani A.;
RT "Mutations of CD40 gene cause an autosomal recessive form of
RT immunodeficiency with hyper IGM.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
CC secreted (isoform II).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=P25942-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P25942-2; Sequence=VSP 006472, VSP 006473;
CC TISSUE SPECIFICITY: B-cells and in primary carcinomas.
CC -!- DISEASE: Defects in TNFRSF5 are the cause of hyper-IGM
CC immunodeficiency type 3 (HIGM3) [MIM:608843]. HIGM3 is an
CC autosomal recessive disorder which includes an inability of B
CC cells to undergo isotype switching, one of the final
CC differentiation steps in the humoral immune system, an inability
CC to mount an antibody-specific immune response, and a lack of
CC germinal center formation.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X60592; CAA43045.1; -;
CC EMBL; AL035662; CAC17670.1; -;
CC EMBL; AJ300189; CAC29424.1; -;
CC EMBL; BC012419; AAH12419.1; -;
CC DR PIR; S04460; A60771.
CC DR PDB; 1CDF; 01-APR-97.
CC DR PDB; 1FLL; 18-OCT-00.
CC DR PDB; 1LOA; 08-FEB-00.
CC DR PDB; 1CZ2; 26-SEP-01.
CC -----
CC Query Match 14.6%; Score 208.5; DB 1; Length 277;
CC Best Local Similarity 25.7%; Pred. No. 3.2e-10;
CC Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;
CC -----
CC QY 18 CEKVGVQNS--CDNCPG---TFCKYNPV-CKSCPPSTF-SSIGQPNICRCVAG 69
CC Db CREKQVLSNCCSLCQPGQKLVSDCTETETECULPGCESEFLDTWNRTHCHQHKYCDP 85
CC QY 70 Y--FRFKFCSSTHNAECIEGFHCLGPGQTRC--EKDCRPG-----DELTKQGCKT 118
CC Db NLGLRVQKGTSETDTICTCEGWHCTSEACSCVLHRSCTSPGVGKQIATGVSDTICEP 145
CC QY 119 CSLGTF-NDQGTGVCRWTCNSLDGRSVLKTGTTEKDVCGPPVVSFSPSTTISVTEG 177
CC Db CPVGFSNVSSAFERKCHPWTSCETKDLVVOQAGTKNTDVCGPQ----- 189
CC QY 178 GPGCHSLQVLTFLALTSALLALIFITLLSVLKWIRKPPHIFKPKPK-----K 228
CC Db DRLRALVVIPIFGILFAILLVLFVK--KVAKPTNKAPHPKQEPQEIFPDPLPGS 245
CC QY 229 TTGAQAEEDACSCRCPEEG 249
CC Db NTAAPVQETLHGCPVQTQEDG 266
CC -----
CC RESULT 6
CC TR11 HUMAN
CC ID TR11 HUMAN STANDARD; PRT; 616 AA.
CC AC Q9Y606;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tumor necrosis factor receptor superfamily member 11A precursor
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.

DE receptor) (ODFR).
GN TNFRSF11A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179 (1997).
RN [2]
RN FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400 (1998).
RN [3]
RN INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.
RX MEDLINE=98447691; PubMed=9774460;
RA Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steinman R.M.,
RA Choi Y.;
RT "The TRAF family of signal transducers mediates NF-kappaB activation
RT by the TRANCE receptor.";
RL J. Biol. Chem. 273:28355-28359 (1998).
RN [4]
RN VARIANT PEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2
RX ALA-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.
RX MEDLINE=20082806; PubMed=10615125;
RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA Anderson D.M.;
RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT familial expansile osteolysis.";
RL Nat. Genet. 24:45-48 (2000).
CC -1- FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/OPGL: essential for
CC interactions between T-cells and dendritic cells.
CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
CC skeletal muscle, thymus, liver, colon, small intestine and adrenal
CC gland.
CC -1- DISEASE: Defects in TNFRSF11A are the cause of familial expansile
CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant
CC bone disorder characterized by focal areas of increased bone
CC remodelling. The osteolytic lesions develop usually in the long
CC bones during early adulthood. FEO is often associated with early
CC onset deafness and loss of dentition.
CC -1- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone
CC 2 (PDB2) [MIM:602080]; also known as familial Paget disease of
CC bone. PDB2 is a bone remodelling disorder with clinical
CC similarities to FEO. Unlike FEO, however, affected individuals
CC have involvement of the axial skeleton with lesions in the spine,
CC pelvis and skull.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC
CC EMBL; AF018253; AAB86809.1; -

DR HSP; P25942; 1CDF.
DR Genew; HGNC:11908; TNFRSF11A.
DR MIM; 603499; -
DR MIM; 174810; -
DR MIM; 602080; -
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW Disease mutation; Deafness.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 11A.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT TNFR-CYS 4.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT L -> LALLLCALL (in PDB2).
FT /FTid=VAR_011516.
FT L -> LLLCALL (in FEO).
FT /FTid=VAR_011517.
FT A -> V.
FT /FTid=VAR_011518.
FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;
Query Match 14.4%; Score 205.5; DB 1; Length 616;
Best Local Similarity 29.9%; Pred. No. 1.3e-09;
Matches 61; Conservative 25; Mismatches 71; Indels 47; Gaps 11;
QY 28 CDNCPGTFCRK-----YNPVCKSCPPSTF--SSIGGQPNICRYC-----AGYF 71
DB 47 CNKCEPGYMSKCTTTSDSVCLPGDPEYLDWNEEDKLLHKYCDTGKALVAVVAG-- 104
QY 72 RFKFCSTHNAECIEGPH----CLGPQTRCEKDCRPG-----QELIKQG-CKTCS 120
DB 105 -----NSTTPRRCACTAGYHWSQDC---ECCRRNTECAPGLGAQHPQLQANKDTVCPC 155
QY 121 LGTFNDQ-NGTGVCRPTNCSLDGRSVLKTGTETKDVVCGPPVWSFSFSTTISVTPEGGP 179
DB 156 AGYFSDASSTDKCPWTNCTFLGKRVHGHGTEKSDAVCSSSLPARKPNPHVVLPG-- 213
QY 180 GGHSQVITLFLALTSALLLALIF 203
DB 214 ----LILLFPASV--ALVAALIF 231
RESULT 7
TR18_MOUSE
ID TR18_MOUSE STANDARD; PRT; 228 AA.
AC Q35714; Q9JUK1; Q9JUK2; Q9JUK3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein).

GN TNFRSF18 OR GITR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=C3H;
RX MEDLINE=97322352; PubMed=91717197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
RN Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RL [2]
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=BALB/C;
RX MEDLINE=20256302; PubMed=10798444;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Delfino D., Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of mouse GITR, a member of
RT the tumor necrosis factor/nerve growth factor receptor family.";
RL DNA Cell Biol. 19:205-217(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410(2000).
CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By
CC similarity).
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAFs and
CC TRAF6 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and
CC C); secreted (isoform D).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A;
CC Name=B;
CC Name=C;
CC Name=D;
CC isoId=O35714-1; Sequence=Displayed;
CC isoId=O35714-2; Sequence=VSP_006510;
CC Name=C;
CC isoId=O35714-3; Sequence=VSP_006511;
CC Name=D;
CC isoId=O35714-4; Sequence=VSP_006509;
CC -!- TISSUE SPECIFICITY: Preferentially expressed in activated T
CC lymphocytes.
CC -!- INDUCTION: Upregulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC
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CC
CC EMBL; U82534; AAB81243.1;
CC EMBL; AF109216; AAF14231.1;
CC EMBL; AF229432; AAF61566.1;
CC EMBL; AF229433; AAF61567.1;
CC EMBL; AF229434; AAF61568.1;
CC MGD; MGI:894675; Tthrsf18.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR001368; TNFR_c6.
CC SMART; SM00181; EGF; 1.

DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR NGFR 1; FALSE NEG.
DR PROSITE; PS00650; TNFR NGFR 2; FALSE NEG.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 228 TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 18.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT TRANSMEM 154 174
FT FT DOMAIN 175 228 CYTOPLASMIC (POTENTIAL).
FT FT REPEAT 28 61
FT FT REPEAT 62 101
FT FT REPEAT 102 142
FT FT REPEAT 129 44 BY SIMILARITY.
FT FT DISULFID 29 44 BY SIMILARITY.
FT FT DISULFID 62 74 BY SIMILARITY.
FT FT DISULFID 69 82 BY SIMILARITY.
FT FT DISULFID 103 122 BY SIMILARITY.
FT FT DISULFID 116 141 BY SIMILARITY.
FT FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT VARSPLIC 121 228
FT FT ACSFQFPEERGEOTEKCHLGRWP -> KDPAIRGGAVV
FT FT ACSFQFPEERGEOTEKCHLGRWP -> KDPAIRGGAVV
FT FT S (in isoform D).
FT FT /FTID=VSP_006509.
FT FT ETQPPAEVQLSADACSFQFPEERGEOTEKCHLGRWP
FT FT -> VLLQRPSSRRSCQLRLAASSLRNAGSRQKSVI
FT FT WGVGGHEAMSSVPQARRYKTCPAIPLVRAGAMLCPLPWA
FT FT PCSPOQWRKWWYSGELRLGPWAAFLI (in isoform
FT FT B).
FT FT /FTID=VSP_006510.
FT FT ETQPPAEVQLSADACSFQFPEERGEOTEKCHLGRWP
FT FT -> GQLCPREGENVSPQAPHLPOFYRDDPAIRGGAVVS (in
FT FT isoform C).
FT FT /FTID=VSP_006511.
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;
Query Match 14.3%; Score 203.5; DB 1; Length 228;
Best Local Similarity 29.8%; Pred. No. 6.8e-10;
Matches 64; Conservative 26; Mismatches 84; Indels 41; Gaps 10;
QY 54 SIGGQPNQ-----NICRVAGYFRFKFKFCSSTHNAECEI-EGFHCILGPQCTRC 102
DB 22 SVVEPGCGPGKVGQSGNNTCCSLIYAPKEDCP---KERCICVTPEVHCGDPCKICK 78
QY 103 K-DCRPGQELTKQ-----CKTSLGFNDQNGTGVCRPWTNCSLDGRSVLKTGTEK 154
DB 79 HYPQCGQGVESQGDIVFGFRCVACAMGTFS-AGRDGHCRLWTNCSQFGLTFMFGNKT 137
QY 155 DVVCGPVPVSPSTTISVTPEGPGHSLQVLTFLALTSALLLALIFITLFSVLKWI 214
DB 138 NAVCIP-----EPLPEQY-----GH-----LTVFLVMAACIFLITVQLGLHIWQLR 181
QY 215 RKKPHIFQPKTKTGAQEDACSCROPQEEG 249
DB 182 RQHMCPRETQPEAEVQLSA--EDAGSFQFPEERGG 214
RESULT 8
ID TNR4 HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE receptor) (ACT35 antigen) (TAX-transcriptionally activated
DE glycoprotein 1 receptor) (CD134 antigen).
GN TNFRSF4 OR TXGFL.
OS Homo sapiens (Human).

SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschuler R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
RN [4]
RN CHARACTERIZATION.
RX MEDLINE=9223511; PubMed=10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT death in HeLa cells.";
RL J. Biol. Chem. 274:11868-11873(1999).
RN [5]
RN FUNCTION.
RX MEDLINE=20261554; PubMed=10799510;
RA Rooney I.A., Butovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
RT LIGHT-mediated apoptosis of tumor cells.";
RL J. Biol. Chem. 275:14307-14315(2000).
RN [6]
RN INTERACTION WITH TRAF3.
RX MEDLINE=96278943; PubMed=8663299;
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT the lymphotoxin-beta receptor.";
RL J. Biol. Chem. 271:14661-14664(1996).
RN [7]
RN INTERACTION WITH TRAF4.
RX MEDLINE=98289299; PubMed=9626059;
RA Krajewski M., Krajewski S., Zapata J.M., VanArsdale T.,
RA Gascayne R.D., Beren K., McFadden D., Shabaik A., Hough J.,
RA Reynolds A., Cleveland C.V., Reed J.C.;
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RT adult, fetal, and tumor tissues.";
RL Am. J. Pathol. 152:1549-1561(1998).
RN [8]
RN INTERACTION WITH TRAF5.
RX MEDLINE=9812745; PubMed=9511754;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.

CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; L04270; AAA36757.1; -
CC ENBL; BC026262; AAH26262.1; -
CC PIR; I54182; I54182.
CC HSP; P25942; ICDF.
CC Genew; HGNC:6718; LTBR.
CC MIM; 600979; -
CC GO; GO:0007165; P-signal transduction; TAS.
CC InterPro; IPR008063; Fas receptor.
CC InterPro; IPR001388; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 4.
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00650; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 248 POTENTIAL.
FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 124 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 14.1%; Score 202; DB 1; Length 435;
Best Local Similarity 25.7%; Pred. No. 1.7e-09;
Matches 56; Conservative 26; Mismatches 96; Indels 40; Gaps 8;

QY 28 CINCOPGTF-----CRKNPVCKSCPPSTFSSIGQPN-CNICVCAGYFFKPF--CSS 79
DB 59 CSRCPPGYVSAAKSRIRDTVCATCAENSYHWNLYITCOLCRPCDPVWGLEIAPCTS 118
QY 80 THNAECIEGPHCL--GPQCTRCB--KDCRPGQBLT-----KQCKTKSLGTF--ND 126
DB 119 KKTCTCRCPQGMFCFAWALECTHCELLSDCPGTEAELKDEVGKNNHCVCAGHFGNT 178
QY 127 QNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSTTISVTPEPGGHSLOV 186
DB 179 SSFSARCOPHTRCENCGVLVEAPGTAQDDTCKNPLEPLPPMSGTM----- 225
QY 187 LTLFLALTSALLALLLITLLFLSVLKWIRKPFHFKQ 224
DB 226 -----LMLAVLLPLAFLLLATVPSCLWKSHPSLCRK 257

RESULT 10

NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
[2]
RN SEQUENCE FROM N.A., AND VARIANT ARG-196.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Beutinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
[4]
RN SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
RX ARG-301.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RX TISSUE=PNS;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klatschul S.F., Collins F.B., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RN SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
[7]
RN SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
[8]
RN SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21069356; PubMed=11197692;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus.";
RL Genes Immun. 1:501-503(2000).
[9]
RN SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
[10]
RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE=91056048; PubMed=2173696;
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
[11]
RN CHARACTERIZATION.
RX MEDLINE=93016040; PubMed=1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
[12]
RN INTERACTION WITH TRAF2.
RX MEDLINE=94349371; PubMed=8069916;
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
[13]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RX TRAF2.
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2.";
RL Nature 398:533-538(1999).
[14]
RN VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21603988; PubMed=11762942;
RA Morita C., Horiuchi T., Tsukamoto H., Hattori N., Kikuchi Y.,
RA Arinobu Y., Otsuka T., Sawabe T., Harashima S., Nagasawa K., Niho Y.;
RT "Association of tumor necrosis factor receptor type II polymorphism
RT 196R with systemic lupus erythematosus in the Japanese: molecular and
RT functional analysis.";
RL Arthritis Rheum. 44:2819-2827(2001).
[15]
RN VARIANT ARG-196.
RX MEDLINE=22151311; PubMed=12161545;
RA Peral B., San Millan J.L., Castello R., Moghetti P.,
RA Escobar-Morreale H.F.;
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic
RT ovary syndrome and hyperandrogenism.";
CC -!- FUNCTION: Receptor with high affinity for homotrimeric
CC TNF approximately 5-fold lower affinity for homotrimeric
CC TNF1/lymphotxin-alpha. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF
CC receptor 2 mediates most of the metabolic effects of TNF-alpha.
CC -!- SUBUNIT: Bands to TRAF2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -!- PTM: Phosphorylated; mainly on serine residues and with a very low
CC level on threonine residues.

- !- PTM: A soluble form (tumor necrosis factor binding protein 2) is produced from the membrane form by proteolytic processing.
- !- PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to TNF- α and blocks its interactions with receptors.
- !- SIMILARITY: Contains 4 TNFR-Cys repeats.
- !- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
- !- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrel.com/".

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EMBL; M32315; AAA59929.1; --
EMBL; U52185; AAC50622.1; --
EMBL; U52156; AAC50622.1; JOINED.
EMBL; U52157; AAC50622.1; JOINED.
EMBL; U52158; AAC50622.1; JOINED.
EMBL; U52159; AAC50622.1; JOINED.
EMBL; U52160; AAC50622.1; JOINED.
EMBL; U52161; AAC50622.1; JOINED.
EMBL; U52162; AAC50622.1; JOINED.
EMBL; U52163; AAC50622.1; JOINED.
EMBL; U52164; AAC50622.1; JOINED.
EMBL; M55994; AAA36755.1; --
EMBL; AY264804; AAC89076.1; --
EMBL; AY342040; AAP89239.1; --
EMBL; BC052377; AAH53977.1; --
EMBL; S63368; AAB19824.2; --
EMBL; M35857; AAA63262.1; --
EMBL; AB030950; BAA89053.1; --
PIR; A35356; A35356.
PDB; 1CA9; 12-APR-99.
Genew; HGNC:11917; TNFRSF1B.
-----

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Query Match	13.8%;	Score 197;	DB 1;	Length 461;
Best Local Similarity	26.3%;	Pred. No. 4.7e-09;		
Matches	72;	Conservative 33;	Mismatches 99;	Indels 70; Gaps 15;
QY	25	QNSDCNCPQ-----TFCRK-YNPVCKSCPPSPSSI-GGQPNCNIC-RVCAGYFRFKKFC	77	
DBb	51	QMCCKSKSPQAHKVFCTKTSVTDVCDSCDSTVTLWNVPECLSCGRSSDPQVETQAC	110	
QY	78	SSTHNAECIEGFHC-LOPQ--CTRCE--KDCRPGQELTKQG-----CKTCSLGTF-	124	
DBb	111	TREQNRICTCRPGWCALSKQEGCRLCAPLKRCPGPGVARPCTETSDVVCKPCAPGTFS	170	
QY	125	NPQNGTGVCRPWNTCSLDGRSVLKTGTTEKDVVC-----	158	
DBb	171	NTTSSDTCRPHQICNV----VAIPGNASMDAVCTSTPTRSMAPGAVHLPQVSTRSQH	236	
QY	159	--GPPVVSFSPSTTI-----SVTPGEGPGGHSLOVTLFLALTSALLIALIEITLLFSV	210	
DBb	227	TOPTPEFSTAPSFLLPMGCPSPAGSGDGFALPV-GLIVGVTALGLLIIGVNCV--I	283	
QY	211	LKWIRK-----KPHIFKQPFKKTGAQGE	235	
DBb	284	MTQVKKKPLCLOREAKVPPLPADKARGTQGFEOO	317	

RESULT 12	
TI1B_HUMAN	
ID	TI1B_HUMAN
STANDARD;	PET; 401 AA.
AC	C00300; Q60236; Q9UHP4;
DT	28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor
(osteoprotegerin) (osteoclastogenesis inhibitory factor).
TFNR5f11B OR OPG OR OCIF.
Homo sapiens (Human).
Enkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Kidney;
MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derosé M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Clegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Farpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
Cell 89:309-319(1997).
[2]
SEQUENCE FROM N.A.
TISSUE=Lung cancer;
MEDLINE=98151033; PubMed=9492069;
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
Tsuda E., Morinaga T., Higashio K.;
"Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
osteoclastogenesis in vitro.";
Endocrinology 139:1329-1337(1998).
[3]
SEQUENCE FROM N.A., AND VARIANT ASN-3.
TISSUE=Placenta;
MEDLINE=98351569; PubMed=9688283;
Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
"Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
Eur. J. Biochem. 254:685-691(1998).
[4]

SEQUENCE FROM N.A., AND VARIANT ASN-3.
TISSUE=Eye;
MEDLINE=22338257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Ioshiyuki S., Carninci P., Prange C.,
Rosa S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X.G., Gibbs R.A.,
Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[5]
SEQUENCE OF D2-36 AND 378-10.
MEDLINE=98238645; PubMed=9571159;
Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
Morigasa T., Tsuda E., Higashio K.;
"Characterization of monomeric and homodimeric forms of
osteoclastogenesis inhibitory factor";
Biochem. Biophys. Res Commun. 245:382-387 (1998).

[6] RY SEQUENCE OF 22-393 FROM N.A.
 RC TISSUE=Placenta;
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-P.;
 RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
 RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
 RN [7]
 RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
 RX MEDLINE=97312536; PubMed=9168977;
 RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
 RA Morinaga T., Higashio K.;
 RT "Isolation of a novel cytokine from human fibroblasts that
 RT specifically inhibits osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
 RN [8]
 RP TRAIL BINDING.
 RX MEDLINE=98369100; PubMed=9603945;
 RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
 RA Dul E., Appelbaum E.R., Eichman C., Diprinzio R., Dadds R.A.,
 RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
 RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
 RL J. Biol. Chem. 273:14363-14367(1998).
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
 RX MEDLINE=98148058; PubMed=9478964;
 RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
 RA Morinaga T., Higashio K.;
 RT "Characterization of structural domains of human osteoclastogenesis
 RT inhibitory factor.";
 RL J. Biol. Chem. 273:5117-5123(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=21395914; PubMed=11505389;
 RA Hofbauer L.C., Neuber A., Heufelder A.E.;
 RT "Receptor activator of nuclear factor-kappaB ligand and
 RT osteoprotegerin: potential implications for the pathogenesis and
 RT treatment of malignant bone diseases.";
 RL Cancer 92:460-470(2001).
 CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
 CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
 CC lymph node, trachea, adrenal gland, testis, and bone marrow.
 CC Detected at very low levels in brain, placenta and skeletal
 CC muscle. Highly expressed in fetal kidney, liver and lung.
 CC -1- INDUCTION: Upregulated by increasing calcium concentration in the
 CC medium and estrogens. Downregulated by glucocorticoids.
 CC -1- PTM: N-glycosylated. Contains sialic acid residues.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 2 death domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U94332; AAB53709.1; -;
 CC EMBL; AB002146; BAA25910.1; -;
 CC EMBL; AB008822; BAA32076.1; -;
 CC EMBL; AB008821; BAA32076.1; JOINED.
 CC EMBL; BC030155; AAB30155.1; -;
 CC EMBL; AF134187; AAF20168.1; -;

DR HSP; P25942; ICDP.
 DR Genew; HGNC:11909; TNFRSF1B.
 DR MIM; 602643; -; C:extracellular; TAS.
 DR GO; GO:000576; F:cytokine activity; TAS.
 DR GO; GO:0005125; F:receptor activity; TAS.
 DR GO; GO:0004872; F:signal transduction; TAS.
 DR GO; GO:0007165; P:skeletal development; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM0208; TNFR; 4.
 DR PROSITE; PS00017; DEATH DOMAIN; FALSE_NEG.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 ET SIGNAL; 1 21
 ET CHAIN; 22 401 TUMOR NECROSIS FACTOR RECEPTOR
 FT REPEAT 24 62 SUPERFAMILY MEMBER 11B.
 FT REPEAT 65 105 TNFR-CYS 1.
 FT REPEAT 107 142 TNFR-CYS 2.
 FT REPEAT 145 185 TNFR-CYS 3.
 FT REPEAT 198 269 TNFR-CYS 4.
 FT DOMAIN 270 365 DEATH 1.
 FT SITE 400 400 DEATH 2.
 FT DISULFID 41 54 INVOLVED IN DIMERIZATION.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 107 118 BY SIMILARITY.
 FT DISULFID 124 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT DISULFID 166 185 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 3 3 K -> N.
 FT MUTAGEN 400 400 /FTID=VAR 013439.
 FT MUTAGEN 400 400 C->S: ABOLISHES DIMERIZATION.
 FT CONFLICT 263 263 MISSING: ABOLISHES DIMERIZATION.
 SQ SEQUENCE 401 AA; 46040 MW; EDF448B67D86C71E CRC64;
 Query Match 13.2%; Score 188; DB 1; Length 401;
 Best Local Similarity 32.2%; Pred. No. 2.2e-08;
 Matches 47; Conservative 18; Mismatches 65; Indels 16; Gaps 6;
 Qy 28 CDNCQGTFCR-----KYNPVKSCSPSTFS-SIGQPNCLCR-VCAGYFRKFCST 80
 Db 41 CDKCPPTGYLKQKCTAKWTVCAPCPDHYTDSWHTSDCLYCSVPVKELQVVKQCNRT 100
 Qy 81 HNAECCEIEGHCLGPQCTRCCKDCRFGQELTKQG-----CKTSLGTF-NDQNGTV 132
 Db 101 HNRVCECKEGRYLEIEFCLK-HRSCPPGFGVQAGTPERTNCTKRCPCDGFNETSSKAP 159
 Qy 133 CRPWTNCSLDGRSVLKTGTETKDVVC 158
 Db 160 CRKHTNCSVFGLLLTQGNATHDNIC 185
 RESULT 13
 TNRS MOUSE
 ID -TNRS MOUSE STANDARD; PRT; 289 AA.
 AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 5 precursor

(CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
TNFRSF5 OR CD40.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
SEQUENCE FROM N.A. (ISOFORM I).
MEDLINE=92105763; PubMed=1370315;
Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
species of murine CD40 upon B lymphocyte activation.";
J. Immunol. 148:620-626(1992).
[2]
REVISONS.
STRAIN=BALB/c;
Torres R.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
[3]
SEQUENCE FROM C.A. (ISOFORM I).
STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93094586; PubMed=12811194;
Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
J. Immunol. 149:3921-3926(1992).
[4]
SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND V).
MEDLINE=21117110; PubMed=11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through
alternative splicing";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
[5]
INTERACTION WITH TRAF3.
MEDLINE=95194010; PubMed=7533327;
Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
Science 267:1494-1498(1995).
[6]
INTERACTION WITH TRAF5.
MEDLINE=96382484; PubMed=8790348;
Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,
Yamamoto T., Inoue J.-I.;
RT "TRAF5, a novel tumor necrosis factor receptor-associated factor
family protein, mediates CD40 signaling.";
Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
CC -1- FUNCTION: Receptor for TNFSF5/CD40L.
CC SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,
CC TRAF2 and TRAF6 [By similarity].
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV
and V); secreted (isoform II).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=5;
CC Name=I;
CC IsoId=P27512-1; Sequence=Displayed;
CC Names=II;
CC IsoId=P27512-2; Sequence=VSP_006474, VSP_006475;
CC Names=III;
CC IsoId=P27512-3; Sequence=VSP_006477, VSP_006478;
CC Names=IV;
CC IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
CC Names=V;
CC IsoId=P27512-5; Sequence=VSP_006476;
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.

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CC

		or send an email to license@isb-sib.ch).		
CC	EMBL; M83312; AAB0705.1; -;			
CC	EMBL; M94126; AAA37404.1; -;			
DR	EMBL; M94129; AAA37404.1; JOINED.			
DR	EMBL; M94128; AAA37404.1; JOINED.			
DR	EMBL; M94127; AAA37404.1; JOINED.			
DR	EMBL; AJ401387; CAC29427.1; -;			
DR	EMBL; AJ401386; CAC29428.1; -;			
DR	EMBL; AJ401389; CAC29429.1; -;			
DR	EMBL; AJ401390; CAC29430.1; -;			
DR	PIR; A46476; A46476.			
DR	HSSP; P25942; ICDF.			
DR	MGD; MG1:88336; Trnrsf5.			
DR	InterPro; IPR008063; Fas_receptor.			
DR	InterPro; IPR001368; TNFR_CS.			
DR	Pfam; PF00020; TNFR_C6; 4.			
DR	PRINTS; PRO1680; FASRECEPTOR.			
DR	SMART; SMO0208; TNFR; 4.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.			
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal;			
FT	Alternative splicing.			
FT	SIGNAL 1 19	POTENTIAL.		
FT	CHAIN 20 289	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 5. EXTRACELLULAR (POTENTIAL) . POTENTIAL. CYTOPLASMIC (POTENTIAL) . TNFR-CYS 1. TNFR-CYS 2. TNFR-CYS 3. TNFR-CYS 4. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. N-LINKED (GLCNAC...) (POTENTIAL) . SCDKNLEVLQKGTSTNTVCGLKSRMALLVPIPVVMG -> RKFVPDASPAGHSCRDPGHHPHRGVSLYKGQGETKG (in isoform II) . /FTID=VSP_006474. Missing (in isoform II) . /FTID=VSP_006475. GLKSRMRALLVIPVMGILLITIRGVFLYIK -> E (in isoform V) . /FTID=VSP_006476. KVVKPKDEMPLPAARR -> SECSEGEREGFSFVEPA S (in isoform III) . /FTID=VSP_006477. Missing (in isoform III) . /FTID=VSP_006478. KVVKPKP -> SQGETKG (in isoform IV) . /FTID=VSP_006479. Missing (in isoform IV) . /FTID=VSP_006480. /FTID=VSP_006480. SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;		
Query Match	13.1%; Score 186.5; DB 1; Length 289;			
Best Local Similarity	25.1%; Pred No. 2.2e-08;			
Matches	61; Conservative 34; Mismatches 87; Indels 61; Gaps 11;			
Qy	28 CDRCQCQTGFCKRY-----NPVCKSCPPTSFSSIGGGP-QNNICRVCAQY--FFPKPFCS 79			
Db	38 CDLCQPGSRULTSHCTALEKTQCHFCDSGEPSAQNWREIRCHQRHCEPNQGLAVKKEGTA 97			
Qy	80 THNAECIEGFFCLGPQCTRCEK---DCRPP-----QLTKQGCKTCSLGNFNONGMT 130			
Db	98 ESDTVTCCKGQHCTSKDCRACAQHPCLPIFGVGWEMATETTDTVCPCFPVGFPSNOSSL 157			

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CC Name=IV;
CC IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
CC Name=V;
CC IsoId=P27512-5; Sequence=VSP_006476;
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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QY 131 -GVCPRWNCSDGRSVLTKTGTTEKDVCGPPVVSFSPSTTSVTPEGGGHSLOVLT 189
 Db 158 FCEYCPWTSCEKDNLEVLQKTSQTNVICG- - - - -L 188
 QY 190 FLALTSALLALI--FITLFSVLKWRKFKPHKQP--FKKTTGAQDEEDACSCRCPO 245
 Db 189 KSRMRALLVPPVNGILITIFGVFLYIKK-----VKKPKDNEMLPAPARRQD-----PQ 238
 QY 246 EEE 248
 Db 239 EME 241

RESULT 14

TR6B_HUMAN STANDARD; PRT; 300 AA.
 AC 095407;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
 GN TNFRSF6B OR DCR3 OR TR6).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Fetal lung;
 RX MEDLINE=9087326; PubMed=9872321;
 RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA Goddard A.D., Botstein D., Ashkenazi A.;
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RL colon cancer.";
 RL Nature 396:699-703(1998).
 RN [2]
 RC SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
 RP TISSUE=Prostate;
 RX MEDLINE=99253915; PubMed=10318773;
 RA Yu X.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 RT "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 RL J. Biol. Chem. 274:13733-13736(1999).
 RN [3]
 RC SEQUENCE FROM N.A.
 RP TISSUE=lung;
 RX MEDLINE=20122600; PubMed=10655513;
 RA Bai C., Connolly B., Metzker M.L., Halliard C.A., Liu X., Sandig V.,
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
 RT independent of gene amplification and its location in a four-gene
 RT cluster.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 RN [4]
 RC SEQUENCE FROM N.A.
 RP Matthews L.;
 RX Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bozak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT
 CC and TNFSF6/FasL. Protects against apoptosis.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 CC Detected in adult stomach, spinal cord, lymph node, trachea,
 CC spleen, colon and lung. Highly expressed in several primary tumors
 CC from colon, stomach, rectum, esophagus and in SW480 colon
 CC carcinoma cells.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
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 CC -----
 DR EMBL; AF104419; AAD03056.1; -
 DR EMBL; AF134240; AAD29688.1; -
 DR EMBL; AF217796; AAF35244.1; -
 DR EMBL; AF217793; AAF33685.1; -
 DR EMBL; AF217794; AAF33686.1; -
 DR EMBL; AF218454; CAC03668.1; -
 DR EMBL; BC017065; AAH17065.1; -
 DR EMBL; BC034349; AAH34349.1; -
 DR HSP; O14763; IDOG.
 DR Genew; HGNC:11921; TNFRSF6B.
 DR MIM; 603361; -
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR InterPro; IPR001368; TNFR C6.
 DR Pfam; PF00020; TNFR C6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 29
 CHAIN 30 300 TUMOR NECROSIS FACTOR RECEPTOR
 SUPERFAMILY MEMBER 6B.
 FT REPEAT 31 70
 FT REPEAT 72 113 TNFR-CYS 1.
 FT REPEAT 115 150 TNFR-CYS 2.
 FT REPEAT 152 193 TNFR-CYS 3.
 FT REPEAT 195 237 TNFR-CYS 4.
 FT DISULFID 49 62 BY SIMILARITY.
 FT DISULFID 52 70 BY SIMILARITY.
 FT DISULFID 73 88 BY SIMILARITY.
 FT DISULFID 91 105 BY SIMILARITY.
 FT DISULFID 95 113 BY SIMILARITY.
 FT DISULFID 115 126 BY SIMILARITY.
 FT DISULFID 132 150 BY SIMILARITY.
 FT DISULFID 153 168 BY SIMILARITY.
 FT DISULFID 174 193 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;
 Query Match 13.0%; Score 185; DB 1; Length 300;
 Best Local Similarity 28.3%; Pred. No. 3e-08;
 Matches 65; Conservative 24; Mismatches 85; Indels 56; Gaps 14;

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski J., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RX INTERACTION WITH TRAF2 AND TRAF5.
RP MEDLINE=97298041; PubMed=9153189;
RA Hsu H., Solovyev I., Colombero A., Elliott R., Kelley M., Boyle W.J.,
RT "ATAR, a novel tumor necrosis factor receptor family member, signals
RT through TRAF2 and TRAF5.",
RL J. Biol. Chem. 272:13471-13474(1997).
[7]
RX INTERACTION WITH TRAF3 AND TRAF5.
RP MEDLINE=97306297; PubMed=9162022;
RA Masters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
RA Ashkenazi A.,
RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
RT receptor (TNFR) family, interacts with members of the TNFR-associated
RT factor family and activates the transcription factors NF-kappaB and
RT AP-1.",
RL J. Biol. Chem. 272:14029-14032(1997).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
RX MEDLINE=21403268; PubMed=11511370;
RA Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
RA Eisenberg R.J., Wiley D.C.,
RT "Herpes simplex virus glycoprotein D bound to the human receptor
RT HveA",
RL Mol. Cell 8:169-179(2001).
CC -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
CC TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
CC an important role in HSV pathogenesis because it enhanced the
CC entry of several wildtype HSV strains of both serotypes into CHO
CC cells, and mediated HSV entry into activated human T cells.
CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN LUNG, SPLEEN, AND THYMUS.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.

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DR EMBL; U70321; AAB58354.1; -;
DR EMBL; U51232; AAD00505.1; -;
DR EMBL; AF153978; AAF75588.1; -;
DR EMBL; AF373877; AAL47717.1; -;
DR EMBL; AF373878; AAL47718.1; -;
DR EMBL; BC002794; AAO02794.1; -;
DR PDB; 1JMA; 26-SEP-01.
DR Genew; HGNC:11912; TNFRSF14.
DR MIM; 602746; -;
DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
DR GO; GO:0007166; F:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3_
DR PRINTS; PR01650; FASRECEPTOR.
DR SMART; SMO0208; TNFR; 3_
DR PROSITE; PS00852; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW 3D-structure. 1 38 POTENTIAL.

FT CHAIN 39 283 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 39 202 SUPERFAMILY MEMBER 14.
FT TRANSMEM 203 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 224 283 POTENTIAL.
FT REPEAT 42 75 CYTOPLASMIC (POTENTIAL).
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 121 162 TNFR-CYS 2.
FT REPEAT 121 162 TNFR-CYS 3.
FT DISULFID 42 53
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 99 119
FT DISULFID 121 138
FT DISULFID 127 135
FT CARBOHYD 110 110
FT CARBOHYD 173 173
FT VARIANT 17 17
FT VARIANT 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 241 241 K -> R (in dbSNP:4870).
FT VARIANT 241 241 /FTID=VAR_013007.
FT VARIANT 241 241 V > I.
FT VARIANT 241 241 /FTID=VAR_013440.
FT TURN 44 45
FT STRAND 46 46
FT STRAND 49 49
FT STRAND 50 51
FT STRAND 52 52
FT STRAND 55 55
FT STRAND 57 57
FT TURN 59 60
FT STRAND 61 65
FT STRAND 74 77
FT TURN 80 81
FT STRAND 82 83
FT STRAND 88 88
FT STRAND 94 95
FT TURN 101 104
FT STRAND 105 109
FT STRAND 118 121
FT TURN 123 124
FT STRAND 125 129
FT STRAND 137 140
SQ SEQUENCE 283 AA; 30392 MW; 46C13C2C70242C1 CRC64;
Query Match 12.4%; Score 176.5; DB 1; Length 283;
Best Local Similarity 29.9%; Pred. No. 1.4e-07;
Matches 49; Conservative 18; Mismatches 66; Indels 31; Gaps 9;
QY 1 MGNNCYNVVVILLVGCCK-----VCAVQNSCDNCPGTFCKK-----YNPYCKSCPST 51
DB 30 LGAPCY-----APALPSCKDEYFVGS--ECCPKSPGYRVKACGELTGTVCPCPPGT 82
QY 52 F-SSIGGQPNMCNCRVC--AGYFRFKKFCSSSTHNAECIEGPHCL---GPOCTRC--K 103
DB 83 YIAHNGLSKCLCCQCDPAMGLRASENCSRTENAVCGSPGHFCIVQDGDHCAACRAYA 142
QY 104 DCRPGQELTKQG-----CKTCSLCTFNDQNGTGVCRPWTNCS 140
DB 143 TSSPGQGVQKGTESQDTLCQNCPPGTFSPNGTLERCOHQTKCS 186
RESULT 20
TNFR4 RAT
ID TNR4 RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
GN receptor) (OX40 antigen) (MRC OX40).
GN TNFRSF4 OR TXGP1L OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

FT DISULFID 65 81 BY SIMILARITY.
FT DISULFID 84 96 BY SIMILARITY.
FT DISULFID 87 104 BY SIMILARITY.
FT DISULFID 106 117 BY SIMILARITY.
FT DISULFID 112 120 BY SIMILARITY.
FT DISULFID 120 120 BY SIMILARITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 250 AA; 48477C2E0C244697 CRC64;

Query Match 11.9%; Score 169.5; DB 1; Length 250;
Best Local Similarity 27.0%; Pred. No. 4.7e-07;
Matches 62; Conservative 29; Mismatches 94; Indels 45; Gaps 11;

QY 28 CDNCQPGT-CKKYNPV-CKSCPPST-PS-SIGGQPNICRVCAGYFRFKFSS 79
DB 40 CRWCEFTFVKDCEDRTAAQDCIPGTSFDPYHTRPHCESRHCNCSGLIRN-CTV 98
QY 80 THNAECEIEGHCLGPGQTRCEKDCRPGQELTKGCKTCSLGTNDQNGTGVCRPWTNC 139
DB 99 TANAECSCSKWCRDQECTCDPLNPA--LTRQPSSTPSPQ-----PPTH- 144
QY 140 SLDGRSVLTKGTEDKDVCGPPVSPSTTSVTPGPGGSHSLQVLTFLALTSALL 199
DB 145 -----LPHGTEKPSW-----FLHQLPNSVTYSQRSHRPLCSDCIRIFVTFSSMFL 193
QY 200 ALIFITLFLSVLKWIRKPPHIFKOPFKTKTGAQBEDACSCRCPOEEEG 249
DB 194 FVLGALFLHQR---RNHGPNEHQ-----AVPEPCPYSCPREBEG 232

RESULT 23

TNR5_BOVIN
ID TNR5_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN TNR5F5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC !- FUNCTION: Receptor for TNFSF5/CD40L.
CC !- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity).
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U57745; AAC48710.1; -
DR HSSP; P25942; 1CDF.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.

DR SMART; SM00308; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >269 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 5.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37 BY SIMILARITY.
FT DISULFID 38 51 BY SIMILARITY.
FT DISULFID 41 59 BY SIMILARITY.
FT DISULFID 62 77 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 119 BY SIMILARITY.
FT DISULFID 111 116 BY SIMILARITY.
FT DISULFID 125 143 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 746903F30F95F387 CRC64;

Query Match 11.7%; Score 167; DB 1; Length 269;

Best Local Similarity 25.5%; Pred. No. 8e-07; Indels 56; Gaps 13;

Matches 61; Conservative 28; Mismatches 94; Indels 56; Gaps 13;

QY 28 CDNCQPGT-CKKYNPV-CKSCPPST-PS-SIGGQPNICRVCAGYFRFKFSS 81
DB 38 CDLCPPGQKLVNDCTEVSQCKGKGFSLWNRKCYCHEHYRNPGLRISQGL 97
QY 82 NAB--CECTEGFHLGPGQTRCEKDCRPG-----QELTKGCKTCSLGT-NDQNG 129
DB 98 NDTITCVCEGQCHTSHTCESTPHSLCLGFGVKQIATGLDVTCEPCPLGFFNSVSA 157
QY 130 TGVCRPWTNCSDGRSVLTKGTEDKDVCGPPVSPSTTSVTPGPGGSHSLQVLT 189
DB 158 FEKCHRWTSCEKGLVEQVGTNKTDVCG---FQSRMTLVIP----- 199
QY 190 FLALTGALLALIFIT-LLFSVLK-----WIRKFP-----HIKQPKKTGA 232
DB 200 ---VTMGVLFAVLVSGACIRNITKQQLPCTLWLGRIEWRRLIRIPAP-TRLSGA 254

RESULT 24

TNR7_HUMAN
ID TNR7_HUMAN STANDARD; PRT; 260 AA.
AC P26842;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 7 precursor (CD27L
DE receptor) (T-cell activation antigen CD27) (T14).
GN TNFRSF7 OR CD27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=92013149; PubMed=1655907;
RA Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.;
RT "The T cell activation antigen CD27 is a member of the nerve growth
RT factor/tumor necrosis factor receptor gene family.";
RL J. Immunol. 147:3165-3169(1991).
RN [2]
RP SEQUENCE FROM N.A.; AND VARIANT THR-59.
RX MEDLINE=93094588; PubMed=1334106;

RA Loenen W.A., Graveststein L.A., Beumer S., Melief C.J., Hagemeijer A.,
RA Borst J.,
RA "Genomic organization and chromosomal localization of the human CD27
RA gene",
RA J. Immunol. 149:3937-3943 (1992).
RL [3]
RN SEQUENCE FROM N.A.
RP TISSUE=B-cell;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP INTERACTION WITH TRAF2.
RX MEDLINE=9335639; PubMed=9692890;
RA Graveststein L.A., Amesen D., Boes M., Calvo C.R., Kruijsbeek A.M.,
RA Borst J.,
RA "The TNF receptor family member CD27 signals to Jun N-terminal kinase
RA via Traf-2",
RL Eur. J. Immunol. 28:2208-2216 (1998).
RN [5]
RP INTERACTION WITH SIVA.
RX TISSUE=Cervical carcinoma, and Thymus;
RA MEDLINE=9732375; PubMed=9177220;
RA Prasad K.V.S., Ao Z., Yoon Y., Wu M.X., Rizk M., Jacquot S.,
RA Schlossman S.F.,
RA "CD27, a member of the tumor necrosis factor receptor family, induces
RA apoptosis and binds to Siva, a proapoptotic protein",
RL Proc. Natl. Acad. Sci. U.S.A. 94:6346-6351 (1997).
CC -!- FUNCTION: Receptor for TNFSF7/CD27L. May play a role in survival
CC of activated T-cells. May play a role in apoptosis through
CC association with SIVA.
CC -!- SUBUNIT: Homodimer. Interacts with SIVA and TRAF2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found in most T lymphocytes.
CC -!- PTM: Phosphorylated and O-glycosylated (Probable).
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD27 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd27.htm".
CC -----
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CC -----
CC EMBL; M63928; AA58411.1; -;
CC EMBL; BC012160; AAH2160.1; -;
CC PIR; A46517; A46517.
CC HSSP; P19438; INCF.
CC Genew; HGNC:11922; TNFRSF7.
CC MIM; 186711; -;
CC GO; GO:0005886; C:plasma membrane; TAS.
CC InterPro; IPR008063; Fas_receptor.

DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Apoptosis; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Phosphorylation; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 260
FT DOMAIN 21 191
FT TRANSMEM 192 212
FT DOMAIN 213 260
FT REPEAT 26 63
FT REPEAT 64 104
FT REPEAT 105 141
FT DISULFID 27 39
FT DISULFID 40 53
FT DISULFID 43 62
FT DISULFID 65 81
FT DISULFID 84 96
FT DISULFID 87 104
FT DISULFID 106 117
FT DISULFID 112 120
FT CARBOHYD 95 95
FT MOD_RES 219 219
FT VARIANT 59 59
FT SEQUENCE 260 AA; 29156 MW; 43C38B92FA90D4E2 CRC64;
SQ
Query Match 11.7%; Score 166.5; DB 1; Length 260;
Best Local Similarity 25.0%; Pred No. 8.5e-07;
Matches 63; Conservative 25; Mismatches 85; Indels 79; Gaps 12;
QY 28 CMCQPGTF----CRKYNPV--CKSCPPS--TFS--SIGQPNCKVCAGYFRFKKFCSS 79
DB 40 CQCEPGTFLVKDCQHRKAAQDCPCIPGVSPDHTPHSCSCRCNCNGLLVNR-CTI 98
QY 80 THNAECCEIEGHCLGPOCTRCEKCRPOELTKQCKTCSLGTNDQNGTGVCRWTNC 139
DB 99 TANAECACRNGQCRDKECTCD-----SQALSHPPQTHLPYVSEMLEARTAGH-MQLADPQLPA 171
QY 140 SLIDGRVLKGTGTEKDVCGPVPVVSFSPSTT----ISVTPGGGPGHSLQVLTFLAL-- 193
DB 127 SLTARS-----TSALLLALIFTLFSVLKWRKKFPHFKQPFKKTGAQEDAC 239
QY 194 -----TSALLLALIFTLFSVLKWRKKFPHFKQPFKKTGAQEDAC 239
DB 172 RTLSTHWPPQSRSLCSDDFIRILVIFSGMFLVFTLAGALEFLH-ORRYRSNKGESPVPEAE 230
QY 240 SCR--CPQEEEG 249
DB 231 PCRYSCPRREEG 242
RESULT 25
TNFR_MOUSE
ID TNFR4_MOUSE STANDARD; PRT; 272 AA.
AC P47711;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE receptor) (OX40 antigen).
GN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;

[4] SEQUENCE OF 2743-3695 FROM N.A.
 RP TISSUE=Placenta;
 RC MEDLINE=97415425; PubMed=9271224;
 RX Durkin M.E., Loeschel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
 RA Wewer U.M.,
 RA "tissue-specific expression of the human laminin alpha-chain, and
 RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
 RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
 RL FEBS Lett. 411:296-300(1997).
 RN [5]
 RP EXPRESSION IN RETINA.
 RX MEDLINE=20422761; PubMed=10964957;
 RA Libby R.T., Champilaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
 RA Koch M., Burgess R.E., Hunter D.D., Brunken W.J.;
 RA "Laminin expression in adult and developing retinae: evidence of two
 RT novel CNS laminins";
 RL J. Neurosci. 20:6517-6528(2000).
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -!- SUBUNIT: Laminin-5 complex is an heterotrimer composed of three
 CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
 CC disulfide bonds into a cross-shaped molecule comprising one long
 CC and three short arms with globules at each end.
 CC -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -!- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
 CC muscle, pancreas, retina and placenta. Little or no expression in
 CC brain and liver.
 CC -!- DOMAIN: Domain G is globular and is part of the major cell-binding
 CC site located in the long arm of the laminin heterotrimer.
 CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -!- SIMILARITY: Contains 22 laminin EGF-like domains.
 CC -!- SIMILARITY: Contains 2 laminin IV domains.
 CC -!- SIMILARITY: Contains 5 laminin G-like domains.
 CC -----
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 CC -----
 CC EMBL; AL354836; CAC22309.1; ALT_SEQ.
 CC EMBL; AL354836; CAC22310.1; -
 CC EMBL; AB067494; BAB67800.1; -
 CC EMBL; AB011105; BAA25459.1; -
 CC EMBL; Z95636; CAB09137.1; -
 CC HSSP; P02468; 1KLO.
 CC Genew; HGNC:6485; LAMAS.
 CC MIM; 601033; -
 CC InterPro; IPR008985; ConA like_lec_gl.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR008212; Lam_N2.
 CC InterPro; IPR000034; Laminin_B.
 CC InterPro; IPR002049; Laminin_EGF.
 CC InterPro; IPR001791; Laminin_G.
 CC InterPro; IPR008211; LamNT.
 CC Pfam; PF00052; laminin_B; 1.
 CC Pfam; PF00053; laminin_EGF; 18.
 CC Pfam; PF00054; laminin_G; 2.
 CC Pfam; PF00055; laminin_Nterm; 1.
 CC PRINTS; PR00011; EGF_LAMININ.
 CC ProDom; PD002082; Lam_N2; 1.
 CC ProDom; PD003031; Laminin_B; 1.
 CC SMART; SM00180; EGF_Lam; 20.
 CC SMART; SM00281; LamB; 1.
 CC SMART; SM00282; LamG; 5.
 CC SMART; SM00136; LamNT; 1.
 CC PROSITE; PS00022; EGF_1; 19.

DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
 FT SIGNAL 1 35
 FT CHAIN 36 3695
 FT LAMININ ALPHA-5 CHAIN.
 FT LAMININ N-TERMINAL (DOMAIN VI).
 FT DOMAIN 36 399
 FT LAMININ EGF-LIKE 1.
 FT DOMAIN 300 358
 FT LAMININ EGF-LIKE 2.
 FT DOMAIN 359 428
 FT LAMININ EGF-LIKE 3.
 FT DOMAIN 429 474
 FT LAMININ EGF-LIKE 4.
 FT DOMAIN 494 540
 FT LAMININ EGF-LIKE 5.
 FT DOMAIN 541 586
 FT LAMININ EGF-LIKE 6.
 FT DOMAIN 587 631
 FT LAMININ EGF-LIKE 7.
 FT DOMAIN 632 676
 FT LAMININ EGF-LIKE 8.
 FT DOMAIN 677 722
 FT LAMININ EGF-LIKE 9.
 FT DOMAIN 723 775
 FT LAMININ EGF-LIKE 10.
 FT DOMAIN 776 828
 FT LAMININ EGF-LIKE 11 (INCOMPLETE).
 FT DOMAIN 829 850
 FT LAMININ DOMAIN IV 1 (DOMAIN IV B).
 FT DOMAIN 851 1437
 FT LAMININ EGF-LIKE 12.
 FT DOMAIN 1438 1483
 FT LAMININ EGF-LIKE 13.
 FT DOMAIN 1484 1597
 FT LAMININ EGF-LIKE 14.
 FT DOMAIN 1528 1576
 FT LAMININ EGF-LIKE 15.
 FT DOMAIN 1577 1627
 FT LAMININ EGF-LIKE 16 (N-TERMINAL).
 FT DOMAIN 1628 1637
 FT LAMININ DOMAIN IV 2 (DOMAIN IV A).
 FT DOMAIN 1638 1830
 FT LAMININ EGF-LIKE 17.
 FT DOMAIN 1831 1863
 FT LAMININ EGF-LIKE 18.
 FT DOMAIN 1864 1912
 FT LAMININ EGF-LIKE 19.
 FT DOMAIN 1913 1968
 FT LAMININ EGF-LIKE 20.
 FT DOMAIN 1969 2022
 FT LAMININ EGF-LIKE 21.
 FT DOMAIN 2023 2069
 FT LAMININ EGF-LIKE 22.
 FT DOMAIN 2070 2116
 FT LAMININ EGF-LIKE 23.
 FT DOMAIN 2117 2166
 FT LAMININ G-LIKE 1.
 FT DOMAIN 2167 2735
 FT LAMININ G-LIKE 2.
 FT DOMAIN 2736 2929
 FT LAMININ G-LIKE 3.
 FT DOMAIN 2941 3115
 FT LAMININ G-LIKE 4.
 FT DOMAIN 3124 3232
 FT LAMININ G-LIKE 5.
 FT DOMAIN 3240 3513
 FT LAMININ G-LIKE 6.
 FT DOMAIN 3520 3692
 FT LAMININ G-LIKE 7.
 FT DOMAIN 2203 2221
 FT COILED COIL (POTENTIAL).
 FT DOMAIN 2335 2466
 FT COILED COIL (POTENTIAL).
 FT DOMAIN 2510 2670
 FT COILED COIL (POTENTIAL).
 FT SITE 1722 1724
 FT CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 1838 1840
 FT CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 300 309
 FT BY SIMILARITY.
 FT DISULFID 302 322
 FT BY SIMILARITY.
 FT DISULFID 324 333
 FT BY SIMILARITY.
 FT DISULFID 336 356
 FT BY SIMILARITY.
 FT DISULFID 359 368
 FT BY SIMILARITY.
 FT DISULFID 361 393
 FT BY SIMILARITY.
 FT DISULFID 396 405
 FT BY SIMILARITY.
 FT DISULFID 408 426
 FT BY SIMILARITY.
 FT DISULFID 429 440
 FT BY SIMILARITY.
 FT DISULFID 431 447
 FT BY SIMILARITY.
 FT DISULFID 449 458
 FT BY SIMILARITY.
 FT DISULFID 461 471
 FT BY SIMILARITY.
 FT DISULFID 494 506
 FT BY SIMILARITY.
 FT DISULFID 496 515
 FT BY SIMILARITY.
 FT DISULFID 517 526
 FT BY SIMILARITY.
 FT DISULFID 529 538
 FT BY SIMILARITY.
 FT DISULFID 541 553
 FT BY SIMILARITY.
 FT DISULFID 543 560
 FT BY SIMILARITY.
 FT DISULFID 562 571
 FT BY SIMILARITY.
 FT DISULFID 574 584
 FT BY SIMILARITY.
 FT DISULFID 587 599
 FT BY SIMILARITY.
 FT DISULFID 589 605
 FT BY SIMILARITY.
 FT DISULFID 607 616
 FT BY SIMILARITY.

Query Match 9.9%; Score 141.5; DB 1; Length 3695;
 Best Local Similarity 28.2%; Pred. No. 0.0013;
 Matches 51; Conservative 9; Mismatches 44; Indels 77; Gaps 11;
 QY 20 KVGAVQNSCDNCQPGTFCRKYNPVCKSPSTFSSIGGQPNVCNCRVCAGYFRFKKFC-- 77

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Db 2043 KAGVGRCDRCQEGHF-----GFGCGGCRPCA-----CQP 2074
QY 78 -----SSTH--NARCECIEGFHCLGPOCTCEKDCRFGQ-ELTKQGCKTCSLGTENDQNGT 130
Db 2075 AABGSECHQSGGCHCRPG--TWGPGC-----RECAPGYWGLPEQGCRRC-----QCPC 2121
QY 131 GVCPRPT--NCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTIS-----VTEGPGPGHS 183
Db 2122 GRCDPHTGRNC-----PPGLSGRCDTCSQHQVPPVPGPGVGHIS 2161
QY 184 L 184
Db 2162 I 2162

RESULT 27
VT2_SFVKA STANDARD; PRT; 325 AA.
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor soluble receptor precursor (Protein T2).
GN OS
OS Shope fibroma virus (strain Kasza) (SPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OC NCBI_TaxID=10272;
RN [1]
RP MEDLINE=87321103; PubMed=2820128;
RX Upton C., Delange A.M., McFadden G.;
RA "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT telomeric region of the Shope fibroma virus genome.";
RL Virology 160:20-30(1987).
RN [2]
RP FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC -----
DR EMBL; ML7433; -; NOT ANNOTATED_CDS.
DR EMBL; A23727; CAA01687.1; -.
DR PIR; B43692; B43692.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 325
FT REPEAT 27 62
FT REPEAT 53 104
FT REPEAT 105 147
FT REPEAT 148 186

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FT DISULFID 28 39 BY SIMILARITY.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.
FT DISULFID 64 79 BY SIMILARITY.
FT DISULFID 82 96 BY SIMILARITY.
FT DISULFID 86 104 BY SIMILARITY.
FT DISULFID 106 120 BY SIMILARITY.
FT DISULFID 123 146 BY SIMILARITY.
FT DISULFID 129 149 BY SIMILARITY.
FT DISULFID 164 185 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198AVIE CRC64;

Query Match 9.8%; Score 140.5; DB 1; Length 325;
Best Local Similarity 27.6%; Pred. No. 0.00015;
Matches 43; Conservative 12; Mismatches 54; Indels 47; Gaps 8;

QY 28 CDNCQPGTFCRKY-----NPVCKSCPSTF--SSIGQPNCNCR--VCAGYFRFKFCSST 80
Db 40 CASCHPGFYASRLCGPGSNTVCSPCEDGTFASTNHAPACVSCRGPCTGHLSSQPCDRT 99
QY 81 HNAECECIEGFHCLGPOCTCEKDCRFGQBELTKQGCKTCSLGTENDQNGTGVCRPWTNC- 139
Db 100 HDRVCNCSGTNYCL-----LKGQNGCRICAPQTKCP 130
QY 140 ---SLDGRSVLKTGTT--EKDVVCGPPVVSFSPSTT 170
Db 131 AGYGVSGHT--RAGDTLCEK---CPHTYSDSLSP 161

RESULT 28
TR16_CHICK STANDARD; PRT; 416 AA.
ID TR16_CHICK
AC P18519;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE (p/5 ICD) (Low affinity neurotrophin receptor p/5NTR).
GN NGFR OR TNFRSF16.
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90166579; PubMed=2560385;
RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
RA Shooter E.M., Reichardt L.F.;
RT "Structure and developmental expression of the nerve growth factor
RT receptor in the chicken central nervous system.";
RL Neuron 2:1123-1134(1989).
RN [2]
RN SEQUENCE OF 21-416 FROM N.A.
RX MEDLINE=90152140; PubMed=2154393;
RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
RT "Structure and developmental expression of the chicken NGF receptor.";
RL Dev. Biol. 137:287-304(1990).
CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC and NT-4. Can mediate cell survival as well as cell death of
CC neural cells (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC associated cell death executor. Interacts with TRAF2, TRAF4,
CC TRAF6 and PTPN13 (By similarity)
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: N- and O-glycosylated.
CC -!- PTM: Phosphorylated on serine residues.

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DR PIR; D36858; D36858.
DR PIR; D72175; D72175.
DR PIR; T28623; T28623.
DR HSP; O14763; ID0G.
DR InterPro; IP001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 349 SOLUBLE TNF RECEPTOR II.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 65 BY SIMILARITY.
FT DISULFID 68 83 BY SIMILARITY.
FT DISULFID 86 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 17 17 MISSING (IN STRAINS BANGLADESH-1975 AND
FT VARIANT 160 160 H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT VARIANT 165 165 1966 AND SOMALIA-1977).
FT VARIANT 182 182 A -> T (IN STRAINS BUTLER-1952 AND
FT VARIANT 274 274 GARCIA-1966).
FT VARIANT 335 335 E -> K (IN STRAIN SOMALIA-1977).
FT VARIANT 339 339 A -> E (IN STRAIN SOMALIA-1977).
FT VARIANT 339 339 N -> D (IN STRAINS BUTLER-1952 AND
FT VARIANT 339 339 GARCIA-1966).
FT VARIANT 339 339 P -> L (IN STRAINS BUTLER-1952 AND
FT SEQUENCE 349 AA; 38189 MW; D4SD40B5C6E780EF CRC64;

Query Match 9.7%; Score 138; DB 1; Length 349;
Best Local Similarity 22.6%; Pred. No. 0.00025;
Matches 59; Conservative 28; Mismatches 104; Indels 70; Gaps 11;

QY 28 CDNCQGTFC-----RKYNPVCKSPPTFFSIGGQ-PNCNLCR-VCGYRFRKFCST 80
DB 44 CLSCPPGTVASRLCDSKNTQTCTPCGSGFTTNRNHLFACUSCNGRCNSNQVETRSNNT 103
QY 81 HNAECCEIEGFHCL---GPQCTRCCKDCRFGQELATKQG-----CKTCSLGTENDQ-N 128
DB 104 HNRICESPGYVLLKSGSGCKACVSQTKGIGYGVSGHTSVGDVICSQCGFGTYSHTVS 163
QY 129 GTGVCBPWTNCLDGRSVLKTGTEKDVCGPVPVSPFTTISTVTPGGPGGCHSLQVLT 188
DB 164 SADKCEPVNPNFYIDVITLVPVNDTSC-----TRTTTGLSES----- 204
QY 189 LFLALTSALLAL-----ITLLFSLVKWI-----RKKEPHFFK----- 223
DB 205 ---ILTSETITWNHTDCNPVREBYFVSLNKVATSGFTGENRYQNSKVTCLNFEIKC 261
QY 224 ----QPKTKTGAQBEDACS 240
DB 262 NNGKSSFKQLTRAKNDGMS 282

RESULT 30
LMA2_MOUSE
ID LMA2_MOUSE STANDARD; PRT; 3106 AA.
AC Q60675; Q60675; Q64061;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
DE chain).

```

GN OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Embryo, and Heart;
 RX MEDLINE=95316259; PubMed=7795883;
 RA Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,
 Yamada Y.;
 RT "Cloning and expression of laminin alpha 2 chain (M-chain) in the
 mouse.";
 RL Matrix Biol. 14:447-455(1995).
 [2]
 RP SEQUENCE OF 2162-2279 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RX MEDLINE=93346725; PubMed=8345183;
 RA Chang A.C., Wadsworth S., Colligan J.E.;
 RT "Expression of merosin in the thymus and its interaction with
 thymocytes.";
 RL J. Immunol. 151:1789-1801(1993).
 [3]
 RP SEQUENCE OF 64-281 FROM N.A.
 RX MEDLINE=95179178; PubMed=7874173;
 RA Xu H., Wu X.R., Wever U.M., Engvall E.;
 RT "Murine muscular dystrophy caused by a mutation in the laminin alpha
 2 (Lama2) gene.";
 RL Nat. Genet. 8:297-302(1994).
 [4]
 RP SEQUENCE OF 20-25.
 RX MEDLINE=21818471; PubMed=11829758;
 RA Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
 RT "Complete sequence, recombinant analysis and binding to laminins and
 sulphated ligands of the N-terminal domains of laminin alpha3B and
 alpha5 chains.";
 RL Biochem. J. 362:213-221(2002).
 [5]
 RN BINDING TO FELN1, FELN2, AND NID2.
 RP MEDLINE=99146904; PubMed=10022829;
 RX Tait J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
 RA "Binding of the G domains of laminin alpha1 and alpha2 chains and
 perlecan to heparin, sulfatides, alpha-dystroglycan and several
 extracellular matrix proteins.";
 RL EMBO J. 18:863-870(1999).
 [6]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 2932-3106.
 RX MEDLINE=20085745; PubMed=10619025;
 RA Hohenester E., Tisi D., Tait J.F., Timpl R.;
 RT "The crystal structure of a laminin G-like module reveals the
 molecular basis of alpha-dystroglycan binding to laminins, perlecan,
 and agrin.";
 RL Mol. Cell 4:793-792(1999).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 is thought to mediate the attachment, migration and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound
 to each other by disulfide bonds into a cross-shaped molecule
 comprising one long and three short arms with globules at each
 end. The alpha-2 chain is a subunit of laminin-2 (Merosin) and
 laminin-4 (S-merosin). Interacts with FELN1, FELN2 and NID2.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Found in the basement membranes (major
 component).
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domains VI, IV and G are globular.
 CC -1- DISEASE: Defects in LAMA2 are a cause of murine muscular dystrophy
 (dy2u).
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -1- SIMILARITY: Contains 17 laminin EGF-like domains.

DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Major surface-labeled trophozoite antigen 417 precursor.
 DE TSA 417.
 GN Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
 OC NCBI_TaxID=5741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 30957 / WB;
 RX MEDLINE=90280395; PubMed=2352929;
 RA Gillin F.D., Hagblom P., Harwood J., Aley S.B., Reiner D.S.,
 RA McCaffery M., So M., Guiney D.G.;
 RT "Isolation and expression of the gene for a major surface protein of
 RT Giardia lamblia";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4463-4467(1990).
 RN [2]
 RP SEQUENCE OF 480-620 FROM N.A.
 RC STRAIN=AD-1;
 RX MEDLINE=93314970; PubMed=8325510;
 RA Ey P.L., Mayrhofer G.;
 RT "Two genes encoding homologous 70-kDa surface proteins are present
 RT within individual trophozoites of the binucleate protozoan parasite
 RT Giardia intestinalis";
 RL Gene 129:257-262(1993).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- DOMAIN: CONTAINS 29 REPEATS OF THE CXXC MOTIF.
 CC -!- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
 CC
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 CC
 DR EMBL; M33641; AAA02688.1; -;
 DR EMBL; M97488; AAA02581.1; -;
 DR PIR; A35502; A35502.
 DR PIR; PC1294; PC1294.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR005127; Giardia_VSP.
 DR InterPro; IPR009030; Grow_fac_recep.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF03302; VSP; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00261; FU; 3.
 KW Signal; Antigen; Glycoprotein; Transmembrane; Repeat.
 FT SIGNAL 1 17
 FT CHAIN 18 713 MAJOR SURFACE-LABELED TROPHOZOITE
 FT ANTIGEN 417.
 FT DOMAIN 18 679
 FT TRANSMEM 680 708
 FT DOMAIN 709 713
 FT CARBOHYD 289 289
 FT CARBOHYD 676 676
 FT VARIANT 582 582
 FT VARIANT 606 606
 FT SEQUENCE 713 AA; 72510 MW; 9AD7195843DE5601 CRC64;
 Query Match 9.5%; Score 135.5; DB 1; Length 713;
 Best Local Similarity 25.6%; Pred. No. 0.00081;
 Matches 58; Conservative 20; Mismatches 67; Indels 82; Gaps 15;
 QY 15 LVGE-----KVGAVQNSD---NQ-QPGTFCR-----KYNPVCKSPPTFSSIGGQ 58
 DB 312 LVTSACTDGYKPSADKTTCAVSNCKTPG--CKACSGNEGKNEVCDCDGYLTLPTSQ 369
 QY 59 PNC-NICRVACGYF-----REFKFCSSSTHAFCE-----CIEGFHCLGQCRCX 103
 DB 370 ---CIDSCKATGNYGATEGAKLCKECTAANCKTCDGQCGQACNDGFKYNGACSPCH- 426

QY 104 DCRPGQLTKQCKTKCSLGTND-----QNGTGVCRPW 136
 DB 427 -----ESCKTSAGTASDCTECTKALRYGDDGKTCGEGCTTGTGAGACK-- 474
 QY 137 TNCSL--DGRSVLK--TGTE--KDVVCGPPVVSFSPSTTISVTPEG 177
 DB 475 -TCGLTIDGASYCSECATTEYPQNGVCAPKASRATPTCNDSPIQNG 520
 RESULT 32
 LMA2 HUMAN
 ID LMA2 HUMAN STANDARD; PRT; 3110 AA.
 AC P24043; Q14736; Q93022;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 11-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
 DE chain).
 GN LAMA2 OR LAMN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94124633; PubMed=8294519;
 RA Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
 RA Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;
 RT "Human laminin M chain (merosin): complete primary structure,
 RT chromosomal assignment, and expression of the M and A chain in human
 RT fetal tissues";
 RL J. Cell Biol. 124:381-394(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97066955; PubMed=8910357;
 RA Zhang X., Vuolteenaho R., Tryggvason K.;
 RT "Structure of the human laminin alpha2-chain gene (LAMA2), which is
 RT affected in congenital muscular dystrophy";
 RL J. Biol. Chem. 271:27664-27669(1996).
 RN [3]
 RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90238994; PubMed=2185464;
 RA Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E.;
 RT "Merosin, a tissue-specific basement membrane protein, is a
 RT laminin-like protein";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
 RN [4]
 RP VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluf G.A., Amato A.A., Mendell J.R.;
 RT "Novel single base polymorphisms and rare sequence variants in
 RT the laminin 2-chain coding region detected by RNA/SSCP analysis";
 RL Hum. Mutat. 13:174-174(1999).
 RN [5]
 RP ERRATUM.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluf G.A., Amato A.A., Mendell J.R.;
 RL Hum. Mutat. 13:340-340(1999).
 RN [6]
 RP VARIANT MDC1A PRO-2564.
 RX MEDLINE=21476011; PubMed=11591858;
 RA He Y., Jones K.J., Vignier N., Morgan G., Chevallay M., Barois A.,
 RA Estournet-Mathiaud B., Hori H., Mizuta T., Tome F.M.S., North K.N.,
 RA Guicheney P.;
 RT "Congenital muscular dystrophy with primary partial laminin alpha-2
 RT chain deficiency: molecular study";
 RL Neurology 57:1319-1322(2001).
 RN [7]
 RP VARIANTS MDC1A TYR-527 AND ARG-862.
 RX MEDLINE=22439669; PubMed=12552556;

Db 874 SIGSCDLSGSLICKPGTTGR-----YCELCADGVFGDAVDKACQPCRCNAG-GSPSE 928
 QY 76 FCSTHNAECB---ISGPHC-----LGPQCTR-----CEKD-----C 105
 Db 929 VCHS-QTGQCECRANVGQCDCKKAGTFLQSGARGVPCNCNCSFGSKDFCEESQGCW 987
 QY 106 RPOQELKQCKCTCSLTGTFNDQNG-----TGCRPWTNCSDGRSVLTKTGT-BK 154
 Db 988 QPG--VTGKCKDCRCAHGYNFQEGGCTACBCSHLGNCDPKT-----GRICPPNTIGEK 1040
 QY 155 DVVCGPVPVSFSPST 169
 Db 1041 CSKCAPNTWGHSTTT 1055

RESULT 33
 TR16 HUMAN STANDARD; PRT; 427 AA.
 AC P08138;
 DT 01-AUG-1988 (Rel. 08, Last Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
 DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR)
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87051725; PubMed=3022937;
 RA Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
 RA Bothwell M., Chao M.;
 RT "Expression and structure of the human NGF receptor.";
 RL Cell 47:545-554(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [3]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=8906903; PubMed=2850481;
 RA Sehgal A., Patel N., Chao M.;
 RT "A constitutive promoter directs expression of the nerve growth factor
 receptor gene.";
 RL Mol. Cell. Biol. 8:3160-3167(1988).
 RN [4]
 RP INTERACTION WITH TRAF2, TRAF4 AND TRAF6.
 RX MEDLINE=9945585; PubMed=10514511;
 RA Ye X., Mehlen P., Rabizadeh S., Vanarsdale T., Zhang H., Shin H.,
 RA Wang J.J., Leo E., Zapata J.M., Hauser C.A., Reed J.C., Bredesen D.E.;

RT "TRAF family proteins interact with the common neurotrophin receptor
 and modulate apoptosis induction.";
 RL J. Biol. Chem. 274:30202-30208(1999).
 RN [5]
 RP INTERACTION WITH TRAF6.
 RX MEDLINE=99115593; PubMed=9915784;
 RA Khursigara G., Orlinick J.R., Chao M.V.;
 RT "Association of the p75 neurotrophin receptor with TRAF6.";
 RL J. Biol. Chem. 274:2597-2600(1999).
 RN [6]
 RP INTERACTION WITH PTPN13.
 RX MEDLINE=20012928; PubMed=10544233;
 RA Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
 RA Reed J.C., Bredesen D.E., Sato T.A.;
 RT "Functional interaction of Fas-associated phosphatase-1 (FAP-1) with
 p75(NTR) and their effect on NF-kappaB activation.";
 RL FEBS Lett. 460:191-198(1999).
 CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 CC and NT-4. Can mediate cell survival as well as cell death of
 CC neural cells.
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4,
 CC TRAF6 and PTPN13.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: N- and O-glycosylated.
 CC -!- PTM: Phosphorylated on serine residues.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -----
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 CC -----
 DR EMBL; M14764; AAB59544.1; -;
 DR EMBL; BC050309; AAB50309.1; -;
 DR EMBL; M21621; AAA36363.1; -;
 DR PIR; A25218; GCHUN.
 DR HSP; P07174; INGR.
 DR GENE; HGNC:7809; NGFR.
 DR MIM; 162010; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004888; F: transmembrane receptor activity; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death_1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00050; TNFR_NGFR_2; 4.
 DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 KW Repeat; Phosphorylation; Signal.
 FT SIGNAL
 FT CHAIN 1 28
 FT 29 427
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 16.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT TNFR-CYS 1.
 FT TNFR-CYS 2.
 FT TNFR-CYS 3.
 FT TNFR-CYS 4.
 FT DEATH.
 FT SER/THR-RICH.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT DISULFID 47 63
 FT DISULFID 57 83

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FT DISULFID 86 99 BY SIMILARITY.
FT DISULFID 89 107 BY SIMILARITY.
FT DISULFID 109 122 BY SIMILARITY.
FT DISULFID 125 138 BY SIMILARITY.
FT DISULFID 128 146 BY SIMILARITY.
FT DISULFID 149 164 BY SIMILARITY.
FT DISULFID 167 180 BY SIMILARITY.
FT DISULFID 170 188 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 427 AA; 45183 MW; B09FAL43FB3D625B CRC64;

Query Match 9.5%; Score 135; DB 1; Length 427;
Best Local Similarity 25.2%; Pred. No. 0.00054;
Matches 65; Conservative 26; Mismatches 97; Indels 70; Gaps 15;

QY 10 VIVLLVGEKVGAVQ-----NSDNCOPGTF-----CRKYNPVCKSPPS-TFS 53
   : : : : :
Db 15 LLLLLLLVGLGAEACPTGLYTHSGECCKACNLGEGVAPCGANQVCEPCLDSVTFS 74
   : : : : :

QY 54 S-IGQPCNCRVAGYFRKFKCSSTHNAECIEGFHCLGPOCTRCR--KDCRPGQE 110
   : : : : :
Db 75 DVVSATEPCCKTECVGLQSWAPCVAEADDAVCAVGYI--QDTEGRCACRVCEAGSG 133
   : : : : :

QY 111 LF-----XQG--CKTCSLGTENDQ-NGTVGCRPWNCSLDGRSVLKTGTTKDVVC--- 158
   : : : : :
Db 134 LVFSCQDKONTVCRCPDGTVSYDEANHVDPCLPCTVCE-DTERQLRECTRWADAECCEIP 192
   : : : : :

QY 159 -----GPPVVSFS--PSTISVTPEGPG-----GHSIQVLT----- 188
   : : : : :
Db 193 GSWITRTPPEGSDSTAFSTQ---EPEAPPEQDLIASTVAGVVTVMGSSQPVVTRGTTD 249
   : : : : :

QY 189 -----LFLATLSALLALI 202
   : : : : :
Db 250 NLIPVVCSTLAIVVGLV 267

RESULT 34
ID ITB5_PAPCY STANDARD; PRT; 655 AA.
AC Q07441;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Integrin beta-5 (Fragment).
GN ITB5.
OS Papio cynocephalus (Yellow baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9556;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=94040831; PubMed=8224922;
RA Shoji M., Hayzer D.J., Kim T.M., Runge M.S., Hanson S.R.;
RT "Human and baboon integrin beta 5 subunit-encoding mRNAs have
RT alternative polyadenylation sites.";
RL Gene 133:307-308(1993).
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
CC -!- IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC -!- SUBUNIT: HETERO DIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: The cysteine residues are involved in intrachain disulfide
CC bonds.
CC -!- SIMILARITY: Belongs to the integrin beta chain family.
CC -!- SIMILARITY: Contains 2 VWFA-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC -----
CC SBL; L12231; AAA16866.1; -.
DR HSSP; P05106; 1JUV.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR Pfam; PF00362; Integrin_B_1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS00243; INTEGRIN_BETA; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat; Extracellular matrix; Cytoskeleton.
FT DOMAIN 1 575 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 576 598 POTENTIAL.
FT DOMAIN 599 655 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 656 724 VWFA-LIKE.
FT DOMAIN 725 746 4 CYSTEINE-RICH TANDEM REPEATS.
FT REPEAT 321 368 I.
FT REPEAT 369 410 II.
FT REPEAT 411 449 III.
FT REPEAT 450 486 IV.
FT CARBOHYD 203 203 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 510 510 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 561 561 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 655 AA; 72466 MW; BAC3A159CBEL596 CRC64;

Query Match 9.5%; Score 135; DB 1; Length 655;
Best Local Similarity 27.7%; Pred. No. 0.00082;
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;

QY 27 SCNQCQ--PGTFCKYNPVCK---SCP--PSTFSSIGGPGNCRVCAVGYFRKXPCS 78
   : : : : :
Db 385 SCNQCSEFSEFGKIYGFCECDNFSCARNKGVLCSGHGECHGECKHAGYGDNCNC- 443
   : : : : :

QY 79 STHNAEC-----CIEGFHCLGPQC-----TRCEK--DCRPGQELTKGCKTCSL 121
   : : : : :
Db 444 STDISTCRGRDQICSERGHCLGQCQCCTPGAFGEMCEKCPIC-PDACSTKRDVCECP 502
   : : : : :

QY 122 ---GTFNDQNGTVCR---PWTNCSL--DGRSVLKTGTTTEKDVVCGPPVV---SFSPT 169
   : : : : :
Db 503 LHSKGPNDQCHSLCRDEVITWDTIVKDQEAFLCFYKTAQDCVMFTVPELPSKSNL 562
   : : : : :

QY 170 TISVTPGPGGSHSLQVLTFLATLSALLALIPITLLFSLVKWI---RKXF 218
   : : : : :
Db 563 TVLREPE---CGTTPNMTILLAVVGSILLVGLALLAIWKLVTIHDRREF 610
   : : : : :

RESULT 35
ID T10D_HUMAN STANDARD; PRT; 386 AA.
AC Q9UBN6; Q9Y6Q4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10D precursor (Decoy
DE receptor 2) (DCR2) (TNF-related apoptosis-inducing ligand receptor 4)
DE (TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death
DE domain).
GN TNFRSF10D OR DCR2 OR TRAILR4 OR TRUND.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT.
 RC TISSUE=Fetal lung;
 RX MEDLINE=98044290; PubMed=9382840;
 RA Marsters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M.,
 RA Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,
 RA Ashkenazi A.,
 RA "A novel receptor for Apo2L/TRAIL contains a truncated death domain.",
 RL Curr. Biol. 7:1003-1006(1997).
 RN [2]
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS SER-35 AND LEU-310.
 RC TISSUE=Foreskin fibroblast, and Peripheral blood lymphocytes;
 RX MEDLINE=98090091; PubMed=9430226;
 RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.Y., Smith C.A.,
 RA Goodwin R.G.,
 RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against
 RT TRAIL-mediated apoptosis, yet retains an incomplete death domain.",
 RL Immunity 7:813-820(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=98196860; PubMed=9537512;
 RA Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.,
 RA "TRUND, a new member of the TRAIL receptor family that antagonizes
 RT TRAIL signalling.",
 RL FEBS Lett. 424:41-45(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., S.W.,
 RA Fahy J., Helton E., Kettner N., Madan A., Gay L.J., Hulyk S.W.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a
 CC truncated death domain and hence is not capable of inducing
 CC apoptosis but protects against TRAIL-mediated apoptosis. Reports
 CC are contradictory with regards to its ability to induce the NF-
 CC kappaB pathway (According to Ref.1 it cannot but according to
 CC Ref.2 it can induce the NF-kappa-B pathway).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed, in particular in fetal
 CC kidney, lung and liver, and in adult testis and liver. Also
 CC expressed in peripheral blood leukocytes, colon and small
 CC intestine, ovary, prostate, thymus, spleen, pancreas, kidney,
 CC lung, placenta and heart.
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.

CC EMBL; AF029761; AAD03477.1; -
 DR EMBL; AF021232; AAC32765.1; -
 DR EMBL; AF021233; AAC32766.1; -
 DR EMBL; AF023849; AAC52053.1; -
 DR EMBL; EC052270; AAH52270.1; -
 DR HSSP; O14763; 1D4V.
 DR Genew; HGNC:11907; TNFRSF10D.
 DR MIN; 603614; -
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 2.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;
 KW Polymorphism.
 FT SIGNAL 1 55 TUMOR NECROSIS FACTOR RECEPTOR
 FT CHAIN 56 386 SUPERFAMILY MEMBER 100.
 FT DOMAIN 56 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 232 POTENTIAL.
 FT DOMAIN 233 386 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 58 97 TNFR-CYS 1.
 FT REPEAT 98 139 TNFR-CYS 2.
 FT REPEAT 140 180 TNFR-CYS 3.
 FT DOMAIN 340 366 DEATH (TRUNCATED).
 FT DOMAIN 225 228 POLY-VAL.
 FT DOMAIN 246 250 POLY-GLY.
 FT DISULFID 83 96 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 118 131 BY SIMILARITY.
 FT DISULFID 121 139 BY SIMILARITY.
 FT DISULFID 141 155 BY SIMILARITY.
 FT DISULFID 158 172 BY SIMILARITY.
 FT DISULFID 162 180 BY SIMILARITY.
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 182 182 P -> S (in TRAIL-R4-B).
 FT VARIANT 35 35 /FTID=VAR_011417.
 FT VARIANT 310 310 S -> L (in TRAIL-R4-B).
 FT SEQUENCE 386 AA; 41823 MW; 77A93577CAAF2632 CRC64;
 Query Match 9.4%; Score 134.5; DB 1; Length 386;
 Best Local Similarity 22.7%; Pred. No. 0.00054;
 Matches 54; Conservative 29; Mismatches 78; Indels 77; Gaps 11;
 QY 29 DNCQGTGTCRKNPVCKSCPPSTFSSIGGQ--PNCNCRVCAGYFRFKFCSSTHNAECE 86
 Db 81 EECFAGSHRSEYTGACNFCETGVDTIASNNLPSCLLCTCKSGQTKNSCTTTRDTVCQ 140
 QY 87 CIEGFHCLGPOCTCEKDCRCPQELTKGQCTCSIGTENDONGTGVCPW-TNCLDGRS 145
 Db 141 -----CEK-----GSFQKNSPEMCKTCTGCP---RG 165
 QY 146 VLKGTG--TTEKDVVCGPPVSPSTTISVTPEGGPGHSLQVLTFLALTSALLALIF 203
 Db 166 MYKVNCSNTPRSDIKC-----KNESAASSGKTPA-----ABETVTTLGLMASPYHVLII 215
 QY 204 ITLFSVLKWI-----RKKEPHLFKQPFKTTGAAQEEACSCRCQEEGGGGY 255
 Db 216 IIVLVIIILAVVVGFSCKRKFISYVK-----GICS-----GGGGGPE 252
 RESULT 36
 ID ITB5 HUMAN STANDARD; PRT; 799 AA.
 AC P18084;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Integrin beta-5 precursor.
 GN ITGB5.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymic epithelium;
RX MEDLINE=90228356; PubMed=2328726;
RA Ramaswamy H., Hemler M.E.;
RT "Cloning, primary structure and properties of a novel human integrin
beta subunit.";
RL EMBL J. 9:1561-1568(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319111; PubMed=2371275;
RA Suzuki S., Huang Z.S., Tanihara H.;
RT "Cloning of an integrin beta subunit exhibiting high homology with
integrin beta 3 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5354-5358(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91009141; PubMed=2211615;
RA McLean J.W., Vestal D.J., Cheres D.A., Bodary S.C.;
RT "cDNA sequence of the human integrin beta 5 subunit.";
RL J. Biol. Chem. 265:17126-17131(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullady S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyx S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gramwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the integrin beta chain family.
CC -!- SIMILARITY: Contains 2 VWFA-like domains.
CC -----
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CC -----
CC EMBL; X53002; CAA37188.1; .
CC EMBL; M35011; AAA52707.1; .
CC EMBL; J05633; AAA59183.1; .
CC EMBL; BC006541; RAH06541.1; .
CC F01; A38308; A38308.
CC HSSP; P05106; 1JUV.
CC Genew; HGNC:6160; ITGB5.
CC MIM; 147561; .

DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002369; Integrin_Beta.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002035; VWFA.
DR Pfam; PF00362; Integrin_B; 1.
DR PRINTS; P00186; INTEGRINB.
DR PRODOM; P001811; Integrin_B; 1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS00243; INTEGRIN_BETA; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN 2.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
Repeat; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 799 INTEGRIN BETA-5.
FT DOMAIN 24 719 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 720 742 POTENTIAL.
FT DOMAIN 743 799 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 136 378 VWFA-LIKE.
FT DOMAIN 465 630 4 CYSTEINE-RICH TANDEM REPEATS.
FT REPEAT 465 512 I.
FT REPEAT 513 554 II.
FT REPEAT 555 593 III.
FT REPEAT 594 630 IV.
FT DISULFID 28 463 BY SIMILARITY.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 39 75 BY SIMILARITY.
FT DISULFID 49 64 BY SIMILARITY.
FT DISULFID 202 211 BY SIMILARITY.
FT DISULFID 239 300 BY SIMILARITY.
FT DISULFID 401 413 BY SIMILARITY.
FT DISULFID 433 682 BY SIMILARITY.
FT DISULFID 461 465 BY SIMILARITY.
FT DISULFID 476 487 BY SIMILARITY.
FT DISULFID 484 522 BY SIMILARITY.
FT DISULFID 489 498 BY SIMILARITY.
FT DISULFID 500 513 BY SIMILARITY.
FT DISULFID 528 533 BY SIMILARITY.
FT DISULFID 530 563 BY SIMILARITY.
FT DISULFID 535 548 BY SIMILARITY.
FT DISULFID 555 555 BY SIMILARITY.
FT DISULFID 569 574 BY SIMILARITY.
FT DISULFID 571 602 BY SIMILARITY.
FT DISULFID 576 585 BY SIMILARITY.
FT DISULFID 587 594 BY SIMILARITY.
FT DISULFID 608 613 BY SIMILARITY.
FT DISULFID 610 657 BY SIMILARITY.
FT DISULFID 615 625 BY SIMILARITY.
FT DISULFID 628 631 BY SIMILARITY.
FT DISULFID 635 644 BY SIMILARITY.
FT DISULFID 641 690 BY SIMILARITY.
FT DISULFID 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 505 505 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 654 654 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 705 705 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 193 193 T -> A (IN REF. 2).
FT CONFLICT 645 645 L -> P (IN REF. 3).
FT CONFLICT 790 792 MISSING (IN REF. 2).
SQ SEQUENCE 799 AA; 88053 MW; D7E472/CA310512B CRC64;

Query Match 9.4%; Score 134; DB 1; Length 799;
Best Local Similarity 27.7%; Pred. No. 0.0012;
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;
QY 27 SCNCQ--PGTFCKYNPVCK-----SCP--PSFTSSIGGQPNICRCVAGYFRFKFKCS 78

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Db 529 SCNQCSFESEFGKIYCPFCEDNFCARNKGVLCGHCHEGCKCHAGYIGDNCNC- 587
QY 79 STNAECECIEGPHCL-----TRCEK--DCRPGQELTKQGCKTCSL 121
Db 588 STDISCRGRDQICSGERHCLCGQCCTEPGAFGEMCEKCPFC-PDAGSTRKDCVCELL 646
QY 122 ---GTNDQNGTGVCR---PWTNCSL--DGRSVLTKGTTEKDVVCGPPVW---SFSRST 169
Db 647 LHSCKPDNQTCHSLRDEVITVTDIKDDQEAVALCFYKTAQCVMMFYVLPSPGKSNL 706
QY 170 TISVTEGGPGGHSLOVLFLFALTSALLLALIFITLFSVLKWI--RKPF 218
Db 707 TVLUREPE---CGNTPNAMTILLAVVGSILLVGLALLAIWKLLVTHDRREF 754

RESULT 37
CRMB_COWPX
ID CRMB_COWPX STANDARD; PRT; 351 AA.
AC O73559; P87602;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Soluble TNF receptor II precursor (cytokine response modifying protein B).
DE (CRMB1 OR D2L) AND (CRMB2 OR I4R).
OS Cowpox virus (CPV).
OC Viruses; GSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90 / Grishak;
RX MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Satronov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
RT proteins."
RL Virology 243:432-460 (1998).
RN [2]
RN FUNCTION.
RC STRAIN=Brighton red;
RX MEDLINE=94378510; PubMed=8091665;
RA Hu F.O., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
RT secreted form of the type II TNF receptor."
RL Virology 204:343-356 (1994).
CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC the modification of TNF-mediated antiviral processes.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC
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CC
CC EMBL; X94355; CAA64087.2; -
CC EMBL; X94355; CAD90756.1; -
CC DR HSP; O14763; IDOG.
CC DR InterPro; IPR001368; TNFR_c6.
CC DR SMART; SM00208; TNFR_c6; 2.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 351 SOLUBLE TNF RECEPTOR II.

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FT REPEAT 31 67 TNFR-CYS 1.
FT REPEAT 69 110 TNFR-CYS 2.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 67 BY SIMILARITY.
FT DISULFID 70 85 BY SIMILARITY.
FT DISULFID 88 102 BY SIMILARITY.
FT DISULFID 92 110 BY SIMILARITY.
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 351 AA; 38253 MW; 57CAE73EF45ED7C7 CRC64;

Query Match 9.3%; Score 133.5; DB 1; Length 351;
Best Local Similarity 29.5%; Pred. No. 0.00059;
Matches 38; Conservative 14; Mismatches 56; Indels 21; Gaps 8;

QY 28 CDNCPQGTFCRKY-----NPVCKSCPSTPSSIGGQ-PNQCIR-VGAGYRFRKFKCS 78
Db 44 CLSCPFGTYASRLCDSKTNTNTCTPCGSGTFTSRNNHLPACLSGRCDSNQVETRSCN 103
QY 79 STNAECECIEGPHCL---GPOCTRC--EKDCRPGQEL---TKQG---CKTSLGTFNDQ 127
Db 104 TTNRICCAFGYICLLKSSGCKACVSTKIGIGYVSGHSTGVDVCSGCLGIYSHT 163
QY 128 -NGTGVCRP 135
Db 164 VSSADKCEP 172

RESULT 38
TNFR6_PIG
ID TNFR6_PIG STANDARD; PRT; 332 AA.
AC O77736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen
DE (CD95)).
DE TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RA "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD.
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC
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RESULT 39

FT DISULFID 129 147 BY SIMILARITY.
 FT DISULFID 150 165 BY SIMILARITY.
 FT DISULFID 168 181 BY SIMILARITY.
 FT DISULFID 171 189 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;
 Query Match 9.3%; Score 133; DB 1; Length 425;
 Best Local Similarity 25.6%; Pred. No. 0.00078;
 Matches 51; Conservative 20; Mismatches 88; Indels 40; Gaps 11;
 QY 10 VIVLLVGCCKVAVQ-----NSCNCQFGTF-----CRKNVPCKSCPPS-TFS 53
 Db 16 LULLLILGVSSGAKCTSTGLYTHSGECCKACNIGEGVAOPCGANQTVCPCLDNVTFS 75
 QY 54 S-IGGPNPNCICRVAGYFRFKKFCSTHNAECIEGF-----HCLGPQCTRCCK-- 103
 Db 76 DVVSATEPCPKCTECLGLQMSAPCVAEADAVCRCAVGYODEETGHC--EACSVCEVGS 133
 QY 104 -----DCRPGOELTKOGCKTCSLGTENDQ-NGTGVCRPWNCSLDGRSVLKTGTEKDVVC 158
 Db 134 GLVFCQKQNTV---CCECPGTYSDANHVDPCLPCTVCE-PTEROLRECTPWADAEC 189
 QY 159 GPPVVSFSPSTTISVTPEG 177
 Db 190 BEIPGRWIPRSI---PPEG 205
 RESULT 40
 CRMB CAMPS
 ID CRMB CAMPS STANDARD; PRT; 349 AA.
 AC Q8UVA7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Soluble TNF receptor II precursor (cytokine response modifying protein B).
 GN (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
 OS Camelpox virus (strain CMS), and
 OS Camelpox virus (strain M-96).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203172, 203173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMS;
 RX PubMed=11907336;
 RA Gubser C., Smith G.L.;
 RT "The sequence of camelpox virus shows it is most closely related to
 RT variola virus, the cause of smallpox.";
 RL J. Gen. Virol. 83:855-872(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M-96;
 RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
 RA Kerembekova U.Z., Sandyaev N.T., Kutish G.F., Rock D.L.;
 RT "The genome of camelpox virus.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
 CC the modification of TNF-mediated antiviral processes (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC
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DR EMBL; AY009089; AAG37456.1; -;
 DR EMBL; AY009089; AAG37718.1; -;
 DR EMBL; AF438165; AAL73920.1; -;
 DR EMBL; AF438165; AAL73917.1; -;
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 KW Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 349 SOLUBLE TNF RECEPTOR II.
 FT REPEAT 31 65 TNFR-CYS 1.
 FT REPEAT 67 108 TNFR-CYS 2.
 FT DISULFID 32 43 BY SIMILARITY.
 FT DISULFID 44 57 BY SIMILARITY.
 FT DISULFID 47 65 BY SIMILARITY.
 FT DISULFID 68 83 BY SIMILARITY.
 FT DISULFID 86 100 BY SIMILARITY.
 FT DISULFID 90 108 BY SIMILARITY.
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 349 AA; 38064 MW; EA412AF991E087F3 CRC64;
 Query Match 9.3%; Score 132.5; DB 1; Length 349;
 Best Local Similarity 29.9%; Pred. No. 0.00071;
 Matches 38; Conservative 14; Mismatches 56; Indels 19; Gaps 8;
 QY 28 CDNCPGTFEC-----RKNVPCKSCPPSTFFSIGGQ-PNCNCR-VCAGYPRFKFKCSST 80
 Db 44 CLSCPGTYASRLCDSKINTQCTPCSGTFTSRNNHLPACLSCNGCRCDNQVETSCNTT 103
 QY 81 HNAECIEGPHCL---GPOCTRC--EKDCRPQDEL---TKQG---CKTCSLGTEN-DON 128
 Db 104 HNRICESEPGYCIILKGSSGCKACVSTKCGIGYGVSGHTSAGDVICSPGLGTYRTVS 163
 QY 129 GTGVCRP 135
 Db 164 SADKCEP 170
 Search completed: May 5, 2004, 14:38:40
 Job time : 22.1644 secs

07yrl5 canis famil
Q9dhl2 cowpox viru
Q72zy5 gallus gall
Q8jfv6 brachydanio
Q8vc17 mus musculu
Q8uy13 vaccinia vi
Q9llr5 vaccinia vi
Q9wjb4 vaccinia vi
Q72735 cowpox viru
Q80yv6 oncorhynchu
Q8sq34 sus scrofa
Q9pus0 salvelinus
Q9y87 cowpox viru
Q9p97 xenopus lae
Q72762 cowpox viru
Q912m6 rattus norv
Q80yv6 rattus norv
Q8wm2 ovis aries
Q72h3 oncorhynchu
Q57484 gallus gall
Q9jke0 rattus norv
Q8jfu6 brachydanio
Q8lm7 chlamydomon
Q8bz6 mus musculu
Q9dfv0 brachydanio
Q57lll variola vir
Q72761 cowpox viru
Q97448 giardia lam
Q57119 cowpox viru

17 174.5 12.2 274 6 Q7YRL5
18 173 12.1 167 12 Q9DJL2
19 172.5 12.1 186 13 Q72ZY5
20 172 12.0 317 13 Q8JFV6
21 171.5 12.0 196 11 Q8VC17
22 171 12.0 167 12 Q8UYL3
23 169 11.8 186 12 Q9LLR5
24 169 11.8 186 12 Q9WJB4
25 168 11.8 186 12 Q72735
26 168 11.8 285 13 Q9Y87
27 167.5 11.7 278 6 Q8SQ34
28 165.5 11.6 302 13 Q9PUS0
29 163 11.4 186 12 Q9Y87
30 161.5 11.3 401 13 Q9P97
31 161 11.3 167 12 Q72762
32 160 11.2 433 11 Q912M6
33 158 11.1 474 11 Q80YV6
34 155 10.9 277 6 Q8WM2
35 154 10.8 318 13 Q72H3
36 152 10.6 1792 13 Q57484
37 151 10.6 169 11 Q9JKE0
38 151 10.6 235 13 Q8JFU6
39 149.5 10.5 1997 10 Q8LBM7
40 146.5 10.3 573 11 Q8BZU6
41 145 10.2 438 13 Q9DFV0
42 144 10.1 349 12 Q57111
43 143 10.0 322 12 Q72761
44 142.5 10.0 645 5 Q97448
45 142 9.9 347 12 Q57119

ALIGNMENTS

RESULT 1

Q8R037 PRELIMINARY; PRT; 211 AA.
AC Q8R037; (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 9.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBAJ databases.
DR EMBL; BC028507; AAH28507.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
KW Receptor.
SQ SEQUENCE 211 AA; 22452 MW; 1EECA84EA32A8D50 CRC64;

Query Match 81.7%; Score 1166.5; DB 11; Length 211;
Best Local Similarity 82.0%; Pred. No. 1e-111;
Matches 210; Conservative 0; Mismatches 1; Indels 45; Gaps 1;
QY 1 MGNNCYNNVVVILLVGCCKVAVQNSCDNCPGTFCKYKYNPVCKSCPSTSSIGGQPN 60
DB 1 MGNNCYNNVVVILLVGCCKVAVQNSCDNCPGTFCKYKYNPVCKSCPSTSSIGGQPN 60
QY 61 CNICRYCAGYFRFKFKFCSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELKQCKTCS 120
DB 61 CNICRYCAGYFRFKFKFCSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELKQCKTCS 120

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:21 ; Search time 87.6712 Seconds
(without alignments)
921.313 Million cell updates/sec

Title: US-10-067-122B-2

Perfect score: 1428
Sequence: 1 MGNNCYNNVVVILLVGCCK.....DACSCRCPOBEGGGGGYEL 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp archaea.*
- 2: sp bacteria.*
- 3: sp fungi.*
- 4: sp human.*
- 5: sp invertebrate.*
- 6: sp mammal.*
- 7: sp mhc.*
- 8: sp organelle.*
- 9: sp phase.*
- 10: sp plant.*
- 11: sp rodent.*
- 12: sp virus.*
- 13: sp vertebrate.*
- 14: sp unclassified.*
- 15: sp rvirus.*
- 16: sp bacteriapi.*
- 17: sp archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1166.5	81.7	211	11	Q8R037 mus musculu
2	225	15.8	275	11	Q80WM9 mus musculu
3	215.5	15.1	483	13	Q800K7 paralicthy
4	205	14.4	467	13	Q800i0 gallus gall
5	203.5	14.3	250	11	Q8C4K3 mus musculu
6	199	13.9	276	13	Q9DDD2 gallus gall
7	188	13.2	223	4	Q86YK5 mus musculu
8	187	13.1	462	13	Q805B0 gallus gall
9	185.5	13.0	289	11	Q8K2X6 mus musculu
10	183.5	12.9	267	6	Q02764 oryctolagus
11	182	12.7	459	11	Q62327 mus musculu
12	181	12.7	457	4	Q8IVS6 homo sapien
13	180.5	12.6	482	11	Q88734 mus musculu
14	180	12.6	651	13	Q98SM6 gallus gall
15	176.5	12.4	283	6	Q9XS28 cercopithe
16	176	12.3	285	13	Q90W71 oncorhynchu

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QY 121 LGTFNDQGTGVCPRWTNCSLDGRSVLKTGTTKDVCGPPVVSFSPSTTISVTPEGGP 180
Db 121 LGTFNDQGTGVCPRWTNCSLDGRSVLKTGTTKDVCGPPVVSFSPSTTISVTPEGGP 180
QY 181 GHSLOVLTFLALTSALLALIFITLLFSVLKWKIRKFPFHFKQPFKKTGAQAQEDACS 240
Db 181 -----FKXTTGAQAQEDACS 195
QY 241 CRCPOEEGGGGGYEL 256
Db 196 CRCPOEEGGGGGYEL 211

RESULT 2
Q80WM9 PRELIMINARY; PRT; 275 AA.
AC Q80WM9
DT 01-JUN-2003 (T-REMBLrel. 24, Created)
DT 01-JUN-2003 (T-REMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-REMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RA Benencia F., Consejo-Garcia J.R., Courreges M.C., Coukos G.;
RT "Light regulation in a murine model of ovarian carcinoma."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY264405; AAC89081.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004889; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; F:as receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Signal.
FT SIGNAL 1 38 Potential.
SQ SEQUENCE 275 AA; 30171 MW; C4A7EADBEFC0521D CRC64;

Query Match 15.8%; Score 225; DB 11; Length 275;
Best Local Similarity 26.2%; Pred. No. 7.7e-15;
Matches 73; Conservative 31; Mismatches 111; Indels 64; Gaps 13;

QY 3 NNCNVVVVLLVLCCKVGAV-----QNSCDNCQPG-----TFCRKY-NPVCKS 46
Db 18 DNTFLVPCVFLNLLQRLAQPSCRQEBFLVGDCECCMCPNGVHVQVQSEHTGVCAP 77
QY 47 CPPPTFSF-IGGQPCNICRVC--AGYFRFKFCSTHNAECCEIEGFHCL---GPQCT 99
Db 78 CPPTQYTAHANGLSKCLPCGVCDPDMDGLLTQQR-CSSWKDTCVRCIFPGYFCNQDGSCHS 136
QY 100 RC--EKDCRPGQELTKQG-----CKTCSLGTFNQDGTGVCPRWTNCSLDGRSVLKTG 150
Db 137 TCLQHTTCCPGQVRVEKRGTHDQDVTVCADCLGTGTFSLGGTQEECLPWTNCSAFQGEV-RRG 195
QY 151 TTEKDVVCGPPVVSFSPSTTISVTPEGGPGHLSQVLTFLALTSALLALIFITLLFSV 210
Db 196 TNSDTTCCSQVVIYVVS-----ILLPLVIVGAGIAGFLICT----- 232
QY 211 LKWKIRKFPFHFKQPFKKTGAQAQEDACSRCRCPQEEEG 249
Db 233 ----RR---HLHTSSVAKELEPFQEQOENTIRFPVTEVG 264
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RESULT 3
Q800K7 PRELIMINARY; PRT; 483 AA.
AC Q800K7
DT 01-JUN-2003 (T-REMBLrel. 24, Created)
DT 01-JUN-2003 (T-REMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-REMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-2.
GN TNFR-2.
OS Paracithys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C., Kurobe T., Hirono I., Aoki T.;
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis
RT factor receptor superfamily genes from Japanese flounder Paralichthys
RT olivaceus."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080947; BAC65226.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 483 AA; 52227 MW; EE55874A8C7F2085 CRC64;

Query Match 15.1%; Score 215.5; DB 13; Length 483;
Best Local Similarity 25.6%; Pred. No. 1.3e-13;
Matches 70; Conservative 31; Mismatches 99; Indels 79; Gaps 13;

QY 23 AVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSIGQPNCNICRVCAGYFRFKFCSSTHN 82
Db 57 ATESVCKQCDSGQYMEKNYAKCL-----SCNCKSNKG-LQVAQRCSTTR 103
QY 83 ASCECIEGFHCL-----GPQCTRCE--KDCRPGQELTKQG-----CKTCSLGT-NDQN 128
Db 104 TCCVCKPGMYCINDPDNYPACRNYSCRAGYGVSLPGKANSVKELCPDGMFSNTSS 163
QY 129 GTGVCPRWTNCSLDGRSVLKTGTTKDVVC-----GP----- 160
Db 164 NTETCRPHDTC--HGKAVVRKGNITSDTVCEGVAPSSLFDQTTKGPHPGILFSTPRIR 221
QY 161 PVWSPSPSTTISVT-----PEGPGHSLQVLTFLALTSALLALIFI 204
Db 222 STVSTAPDPLUSVASVSDVEVTHTIKSPPYKPPGGS-----LAATAGVGMVGFILLFTAV 277
QY 205 TLLFSVLKWKIRKFPFHFKQPFKKTGAQAQED 237
Db 278 LLVFLCKAVSKDVPTF-QPKVDANGCESDD 308

RESULT 4
Q800IO PRELIMINARY; PRT; 467 AA.
AC Q800IO
DT 01-JUN-2003 (T-REMBLrel. 24, Created)
DT 01-JUN-2003 (T-REMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-REMBLrel. 25, Last annotation update)
DE CD30 protein precursor.
GN CD30.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
```



```
Db 123 EPCKQGFVVAAMAEARTSPCEPAEGTFSNVSSKTEPCHFWTSCSEKGLVWKVGTNT 182
QY 154 KQVVGCPVVSFSPSTISVTTEGPGHSLQVLFLFALTSALLLALIFITLFSVLKW 213
Db 183 SDVIC-----ESSRSLSV-----LIPITAAVTVCLVGIYICLVHTD 221
QY 214 IRKKFPHIFKQ-----PPKTTGAQ-----EDACSCRCPOBEE 248
Db 222 LARRGP---KQAEAPRELVTQQPEEVDFFVQETLLGGQPVQAEEDGKESIAEQE 275

RESULT 7
Q86YK5 PRELIMINARY; PRT; 223 AA.
AC Q86YK5;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 (Fragment).
GN TNFRSF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Zeng Y.;
RT "Transcripts of CD40 isoform in peripheral mononuclear cells.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV225405; RA043990.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001993; Mitochond. carrier.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
FT NON TER
SQ SEQUENCE 223 AA; 24659 MW; 8563C20B8C4E0B1C CRC64;

Query Match
Best Local Similarity 26.4%; Score 188; DB 4; Length 223;
Matches 58; Conservative 31; Mismatches 87; Indels 44; Gaps 10;

QY 18 CEKVGAVNS--CDNCPG-----TFCKYNPV-CKSCPSTF--SSICGQPNICRCVAG 69
Db 26 CREKQYLNSCCSLCPGQKLVSDCTETETELCPGSEFLDTWNRTHCHQHYCDP 85

QY 70 Y--FRFKFCSSTHNAECIEGFHCLGPOCTRC--EKDCRPG-----QELTKQGCKT 118
Db 86 NLGLRVQOKGTSFETDTICTCEGWHCTSEACSVLHRSCTPGVQKIATGVSDICEP 145

QY 119 CSLGTF-NDQNGTGVCRPWNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTISVTPEG 177
Db 146 CPVGFNSVSAFKEKHPWTSCETKDVLVQOAGTKNTDVCVGPQ----- 189

QY 178 GPGGHSILQVLTFLALTSALLLALIFITLFSVLKWIRKK 217
Db 190 -DLRALVVIPIIFILFAILLVLFV-----KKVAKK 221
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RESULT 8
Q805B0 PRELIMINARY; PRT; 462 AA.
AC Q805B0;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-II.
GN TNFR-II.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sayde A.A.;
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayed A., Horuchi H., Furusawa S., Matsuda H.;
RT "Molecular cloning and characterization of chicken Tumor necrosis
RT factor receptor-II (TNFR-II) and Tumor necrosis factor receptor
RT associated factor-5 (TRAF-5) genes.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB101004; BAC55966.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 462 AA; 50141 MW; 8B00A93305414782 CRC64;

Query Match
Best Local Similarity 13.1%; Score 187; DB 13; Length 462;
Matches 65; Conservative 36; Mismatches 117; Indels 52; Gaps 11;

QY 24 VQNSCDNCPG-----TFCKYNPVCKSCPSTSSICGQ-PNCNICR-VCAGYFRFKF 76
Db 43 LKCKCKPQORKAKESCHSVDTKICFLPDTYAVNRSPPQCFACSPCKRGFVENQT 102

QY 77 CSSTHNAECIEGFHCLGPOCTRC-----EKDCRPGQELTKQG-----CKTCSLGT 124
Db 103 CTLSDRICSPPEYCYISKYQNCICKVHKCGRGVRSRGTDSDTDECKCPGTF 162

QY 125 NDQNGTGV-CRPWNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTISVTPEGPGGHS 183
Db 163 SDEESYDTSCTPHTVCTV-----KSAVAGNNVNDTVCHDSVATALEHTAVNPLFSQSTNS 218

QY 184 LQVLT-----LFLALTSAALLALIFITL-----LFSVLK-----WIRKKF 218
Db 219 GEIITQVILNFVPMDSYIIGSVTGFLLVLIIVGLVCLFSKKALAYSQPTGAVDSPF 278

QY 219 PHIFKQPPKVTGAQAQEDACSCRCPOBEE 248
Db 279 SPTEKQCDKKVRNAGSQNSSSS-----EQEEQ 305

RESULT 9
Q8K2X6 PRELIMINARY; PRT; 289 AA.
ID Q8K2X6
AC Q8K2X6;
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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029254; AAH29254.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; P: Fas receptor.
DR InterPro; IPR001005; Myb DNA binding.
DR InterPro; IPR01885; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00037; MYB 1; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;

Query Match 13.0%; Score 185.5; DB 11; Length 289;
Best Local Similarity 25.1%; Pred. No. 9.3e-11;
Matches 61; Conservative 33; Mismatches 88; Indels 61; Gaps 11;

QY 28 CDNCQGTGTCYK-----NPVCKSCPPSTFSSIGGQP-NCNICRVGAGY--PRFKFCSS 79
DB |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
38 CDLCQGSRLTSHCTALEKTCQCHPCDSGEPSAQWNRHCHQHRHCEPNQGLVKKEGTA 97
QY 80 THNAECIEGFHCLGQCTRCCK--DCRPG-----QELTKQCKTSLGFNDQNGT 130
DB |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
98 ESDTVCAKGEQCHTCKDCACQAQHTPCIFGFGWEMATETTDTVCHPCVGVGFSSQSSL 157
QY 131 -GVCPRWTCNSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPGPGGHSGLQVLTL 189
DB |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
158 FEKCYPTWSCDKNLEVLQGTSTNVICG-----L 188
QY 190 FLATSAALLALI--FTLLPSVLKWKIRKXPHIFKQPPFK--TTGAAQBEDACSCPCQ 245
DB :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
189 KSRMRALLVFPVWVGILITIFGVLYIKK---VVKPKDNEILPPAARQD-----PQ 238
QY 246 EEE 248
DB |||||
239 EME 241

RESULT 10
002764
ID 002764 PRELIMINARY; PRT; 267 AA.
AC 002764;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUN-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE OX40 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

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OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Seto A.;
RT "Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -
DR HSSP; Q92956; LOMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6; 3.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Signal.
FT NON TER 1 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 267 OX40.
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;

Query Match 12.9%; Score 183.5; DB 6; Length 267;
Best Local Similarity 27.8%; Pred. No. 1.4e-10;
Matches 77; Conservative 22; Mismatches 103; Indels 75; Gaps 17;

QY 9 VVIVLLVGCCK---VGAV-----QNSCDNCQPG-----TFC-RKYNPVCKSCPESTFSSI 55
DB :|||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
10 LLLGLLLGAPRPDCVGDTPYGGDRCCLEQCPGYGMVSRNCRNSQDTICHPCPCGFYNEA 69
QY 56 GQPNQNICRVGAGYFRPKFKCSTHNAECIEGFHCLGQCTRCCKDCHPG-QELT-- 112
DB |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
70 VNYQACKPCTQC-----NRRSGEPQOECT-----HTRDTVCR-----CRPGTQPLNGY 113
QY 113 KQG--CKTCSLGTENDQNGTGVCRPWTCNSLDGRSVLKTGTTEKDVVCG----- 158
DB |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
114 KHGVDCAPCPQGHFSEGNR-ACRPWNTCTLAGRTIQPASSISDAVCEDRSSLATQPWE 172
QY 159 -----GPPVVSFS-----PSTTISVTPGPGGHSGLQVLTLFLATSAALLALIIF 203
DB |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
173 TPSAPYRPPTARTSTAWPRTAQGPSTP---TLEASKGPQLAIVLSGLGLGLALLAAL- 228
QY 204 ITLLPSVLKWKIRKFP--HIFKQPPKKTGAAQBEDA 238
DB |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
229 LALYLHQRAWRPPLPGGSGFRTPI-----QEEQA 258

RESULT 11
002327
ID 002327 PRELIMINARY; PRT; 459 AA.
AC 002327;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Murine tumour necrosis factor receptor 2 protein (Fragment).
GN TNFRSF1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor Necrosis factor receptor 2 is linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor

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KW	Receptor.
FT	NON TER
SQ	SEQUENCE
	1 1
	457 AA; 48120 MW; 1B634BBF1F5D77AC CRC64;
Query Match	12.7%; Score 181; DB 4; Length 457;
Best Local Similarity	25.4%; Pred.No.4.4e-10;
Matches	71; Conservative 36; Mismatches 102; Indels 70; Gaps 15;
Qy	20 KVGAVQNSCDNCPG---TFCKK-KNPVCKSPPTSSSI-GGOENCMNIC-RVCAGYFR 72
Db	42 RTGALGGARLAPPGHAKVFCTKTSDTVCDSCSDSTYTQLMNNWPCELCSCGRCSDDQV 101
Qy	73 FKFKCSTTNAAECIEGHFC-LGPQ--CTRCE--KDCRPGQELTKQG-----CKTCS 120
Db	102 ETOACTREQNRICTCRFGMYCALSKOEGRCRLCAPLKRCSPGFVARPPGTSETSDVVCKPCA 161
Qy	121 LGTF-NDQNGTGVRWTNCSLDGRSVLTKGTTEKDVC-----158
Db	162 PGFSNTTSTDICRHQICNV----VAIPGNASMDAVCTSTPRTSMAPGVHLPQPV 217
Qy	159 -----GPFVVSFPSTTI-----SVTPEGPGGHSLOVITLFLATLSALLALIFIT 205
Db	218 TRSQHTOPTPEPSTARBSTSFLPMGSPPAEGSGDFALPV-GLIVGTALGLLIIGVN 276
Qy	206 LIFSVLKWIRK-----KPHFIKKQFFKTTGAQE 235
Db	277 CV--IMTVQVKKLCLOREAKVPHPADKARGTQGPQQ 313
RESULT 13	
O88734	
ID	O88734 PRELIMINARY; PRT; 482 AA.
AC	O88734; 1
DT	01-NOV-1998 (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	P80 TNF-alpha receptor.
GN	TNF2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON	[1]_TaxID=10090;
RX	NCBI_TaxID=10090;
RP	SEQUENCE FROM N.A.
RP	MEDLINE=98414512; PubMed=9740674;
RA	Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT	"The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
RT	and Characterization of the two Transcripts.";
RL	Genomics 52:79-98(1998).
DR	EMBL; Y14619; CAA74969.1; JOINED.
DR	EMBL; Y14620; CAA74969.1; JOINED.
DR	EMBL; Y14621; CAA74969.1; JOINED.
DR	EMBL; Y14622; CAA74969.1; JOINED.
DR	EMBL; Y14623; CAA74969.1; JOINED.
DR	EMBL; Y14679; CAA74969.1; JOINED.
DR	HSSP; Q92956; IJMA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPRO01368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 4.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
DR	PROSITE; PS00050; TNFR_NGFR_2; 3.
DR	Receptor.
SQ	SEQUENCE 482 AA; 51106 MW; F6C15046B48FFB3C CRC64;
Query Match	12.6%; Score 180.5; DB 11; Length 482;
Best Local Similarity	25.6%; Pred.No.5.2e-10;
Matches	75; Conservative 25; Mismatches 110; Indels 83; Gaps 14;
Qy	25 QNSCDNCPG-----TFCRYKNPVCKSCPPTSSISGGQ-PNCNIC-RVCAGY 70
Db	52 QMCAKCPGQYVXHFCNKTSDTVCAUSDTCVADCEASMTYVMNQVPTCLSCSSCSTD 111


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QY 71 FRFKFCSSTHNAECIEGPHCL-----GPQTRCEKDCRPGQELTKOG-----C 116
DB 112 QVETRACTKQNRVACAGRYCALKTHTSGSCRCQWRLSK-CGPGFGVASSRAPNGNVL 170
QY 117 KTCSLGTEND-QNGTGVCRPWTNCSLDGRSVLTKTGTTEKDVVCGP--PWVSFSPSTTISV 173
DB 171 KACAPGTSDDTSSDVCNRPKICSI-----LAIPGNASTDAVCAPESPTLSAIPRTLVS 226
QY 174 TP-----EGGP-----GHSLOVLTFLALTSALLALI 202
DB 227 QEPTRSQPLDQPGSPQSPSILTSILGSPITTEQSTKGGISLPI-GLIVGVTS---LGLL 282
QY 203 FTLLPSVLKWKTKKPHFKPPKTKTGAOEEADACSCRCPOBEGGGGYE 255
DB 283 MLGLVNCFLVORRKKP-----SCLQDRAKVPVDEKSDQAVGLE 323

RESULT 14
Q98SM6
ID Q98SM6 PRELIMINARY; PRT; 651 AA.
AC Q98SM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OX NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RP Bridgman J.T., Johnson A.L.;
RA "Expression of DR6 in the ovary";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.2; -.
DR FJ; JG7705; JG7705.
DR HSP; P19438; INCF.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00208; TNFR_c6; 1.
DR SMART; SM00208; TNFR_c6; 1.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;

Query Match 12.6%; Score 180; DB 13; Length 651;
Best Local Similarity 30.6%; Pred. No. 8,1e-10;
Matches 49; Conservative 22; Mismatches 71; Indels 18; Gaps 7;

QY 28 CDNCQPGTFCRKYNP-----VCKSCPESTFSS-IGGQPNICR-VCAGVFRFKFCST 80
DB 52 CDKCPAGTVYSKCTKSTLRECSPCDGTFTKHENGIERCHPCRKPCELPMIEKTHCTAL 111
QY 81 HNAECIEGPHCLGPGCTCEKDCRPGQELTKOG-----CKTCSLGTEND-QNGTGV 132
DB 112 TDRECTCLSGTFQINDCVPTV-CPVGNGVRKGTETEDVRCKPCLRGTFSDVPSSVMK 170

QY 133 CRPWTNCSLDGRSVLTKTGTTEKDVVCGPPVVSFSTTIS 172
DB 171 CKTYTDCGKNVWVKGTESDNCVCGSP--ASLPTSLT 208

RESULT 15
Q9XSZ8
ID Q9XSZ8 PRELIMINARY; PRT; 283 AA.
AC Q9XSZ8;
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DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE HVEAS.
GN Cercopithecus aethiops (Green monkey) (Grivet).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=9296730; PubMed=10366573;
RA Foster T.P., Chouljenko V.N., Kousoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein.";
RL Virology 258:365-374 (1999).
DR EMBL; AF147720; AAD37381.1; -.
DR HSP; Q92956; LGMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match 12.4%; Score 176.5; DB 6; Length 283;
Best Local Similarity 24.0%; Pred. No. 7.6e-10;
Matches 66; Conservative 32; Mismatches 100; Indels 77; Gaps 12;

QY 1 MGNMNYVIVVILLVNGCEK-----VGAVQNSCDNCQPGTFCR-----KYNPVCKSCPST 51
DB 30 LGSSCY-----APALPSCKEDEVFVGS--ECCPKCGFGFHVRCAGCEQTGTVCPSPSGT 82
QY 52 F-SSTGGOPNINICRVG--AGVFRFKFCSTHNAECIEGPHCL---GPQTRCE--K 103
DB 83 YIAHFNGLSKLQCCQDCDPAMGLRTRNCSTANALCCSGHFCIIODGDHCAACRAYA 142
QY 104 DCRPGQELTKOG-----CKTCSLGTENDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDV 156
DB 143 TSSPGQVRQKGTESQDITLQCNCPGPTSSNGTLEECQGNKCKS----- 187
QY 157 VCGPPVVSFSPSTTISVTPEGGPGHSLQVLTLEI--ALTSALLALIFITLLPSVLXWI 214
DB 188 -----WLVTGAPGPTSSRWVWLLSGSLIVIVGLIILILICVKR-- 230
QY 215 RKFPFHPKQPPKTTGAAQEDACSCRCPOBEEG 249
DB 231 -----RKSQGDVWVIVSVQRKQEAEG 253

RESULT 16
Q90W71
ID Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OX NCBI_TaxID=8022;
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OX NCBI_TaxID=9031;
RN
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT 'ck3 expression in the hen.';
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251406; AAP03889.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00552; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 186 AA; 20671 MW; 31D65731DACEB758E CRC64;

Query Match 12.1%; Score 172.5; DB 13; Length 186;
Best Local Similarity 28.8%; Pred. No. 1.3e-09;
Matches 46; Conservative 23; Mismatches 66; Indels 25; Gaps 8;

OY 9 VVIVLLVGCERKVGAVQ-----NSCDNCQPGTF-----CRKYNP-VCKSPPPGTFSS 54
DB 20 LLLMLAEIGCSSPPYQWRDAGTKERVTCQCPGTFVAQCHYKERTVTCAPCPDLHYTH 79
OY 55 ICGQ-PNCNCRVAGYPRFK-KFCSTHNAECIEGFCGLGPOCTRCCKRCRPGQELT 112
DB 80 YNNYLEKLCVNVGQERQVQVCNATHNRACQCEGFAEMFCVQ-HSEXPGRSGV 138
OY 113 KQG-----CKTCSLGLFF-NDQNGTGVCRWNTNCSLDGR 144
DB 139 KLGSPSENTQCRACPRGFSFSSSSSTFPCRAHQNTQLGK 178

RESULT 20
Q8JFV6
ID Q8JFV6 PRELIMINARY; PRT; 317 AA.
AC Q8JFV6
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE SI:0107D16.1 (Novel protein similar to vertebrate nerve growth factor receptor (NGFR)) (Fragment).
GN SI:0107D16.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN
RP SEQUENCE FROM N.A.
RA Ramsay H.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL591671; CAD43421.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00552; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
FT NON_TER
SQ SEQUENCE 317 AA; 34446 MW; D9B7EF1C70DAF92B CRC64;

Query Match 12.0%; Score 172; DB 13; Length 317;
Best Local Similarity 23.1%; Pred. No. 2.5e-09;
Matches 65; Conservative 38; Mismatches 96; Indels 82; Gaps 14;

OY 29 DNCQPGTFCRKNPVCKSCPP-----STFS-SIGQPNCRV 66

DB 15 EECSSGSTHS-GECCVQCPGEGVKECGATQTECTQCLDSETFSTFSTHTDKCQVCTE 73
OY 67 CAGYFRFKFCSTHNAECIEGF--HCLGPOCTRCCKRCRPGQ-----ELTKQG-CK 117
DB 74 CTGLMRMTPTCDSNDAAECVNYGFNMVLSRSSRCEPCTV-CPLGQGVDMRCCLNHDVTCE 132
OY 118 TCSLGTENDQGT-GVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVPSPSTTISVTPE 176
DB 133 ECRDETYSQDENTWPCMPCTICEEDTEILLRNCTPTEDALCHDPL---SFTYPTSTGDS 189
OY 177 G-----QPG-----GHSQVLTLFLALTSALLLALIFITLLF 208
DB 190 GSFTDLDRLWSPSPGDDATTPKSPSPHFIFGRGLNENLIPIYCSILAAVVVGL----- 242
OY 209 SVLKWIRKFPFIKQ--PFKTTGAAQEEADACSCRCPOEE 247
DB 243 --LAVI-----IPKWNCKQKQKQANNAATANTPSP 275

RESULT 21
Q8VC17
ID Q8VC17 PRELIMINARY; PRT; 196 AA.
AC Q8VC17
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022125; AAH22125.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260E8 CRC64;

Query Match 12.0%; Score 171.5; DB 11; Length 196;
Best Local Similarity 27.2%; Pred. No. 1.7e-09;
Matches 62; Conservative 22; Mismatches 87; Indels 57; Gaps 11;

OY 35 TFCRKNPVCKSCPPSTFSSIGQPNCRVAGYFRFKFCSTHNAECIEGFCGL 94
DB 2 TYTAHANGLSKCLP-----CGVCDPDMGLLTWQE-CSSWKDTVCRCIPGYFCE 48
OY 95 ---GPOCTRC--EKDCRPGQELTKQG-----CKTCSLGTENDQNGTGVCRWNTNCSLD 142
DB 49 NQDGSCHSTCLQHTTCPPGQVEKRGTHDQDTCADCLTGTFSLGGTQBECLPWTNCSAF 108
OY 143 GRSVLKGTGTEKDVVCGPPVVPSPSTTISVTPEG-OPGHSLOVLTFLALTSALLAL 201
DB 109 QQEV-REGTNSTDTTSCSSQVYVVSILFLVTVGVGIAG-----FLICTRRLHT- 158
OY 202 IFITLLPSVLKWKIRKFPFIKQPFKKTGAAQEEADACSCRCRCPOEEG 249
DB 159 -----SSVAKEL-----EPFQ-----QEQQENTIRFPVTEVG 185

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RESULT 22
Q8UYL3
ID Q8UYL3 PRELIMINARY; PRT; 167 AA.
AC Q8UYL3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CrMe protein.
GN CRME
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USSR;
RA Reading P.C., Khanna A., Smith G.L.;
RT "Vaccinia virus CrMe encodes a soluble and cell-surface tumor necrosis
RT factor receptor that contributes to virus virulence.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ3115962; CAC83048.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 167 AA; 18510 MW; 3B4A0D4A27FB797D CRC64;

Query Match 12.0%; Score 171; DB 12; Length 167;
Best Local Similarity 30.7%; Pred. No. 1.6e-09;
Matches 50; Conservative 22; Mismatches 57; Indels 34; Gaps 9;

QY 9 VVIVL-----LLVGEKVGAVQNS-----CDNCQPGTF-----CRKY-NPVCKSCPP 49
Db 4 VVILGLPIINTSLSMKCEGVSYNSQELKCKLCKPGTYSYDHRCKYSDICGHCPS 63
QY 50 STFSI-CGQPNICRVAGYFFKFP-CSTNNAECIEGPHCL-----GPOCTCEK 103
Db 64 DTFTSYNRSWCHSCRGPGCTGVEVPTCTPTTNRICHDSNSYCLLKASDGNVTCAP 123
QY 104 DCRPQELTKQ-----CKTCSLGTEND-ONGTGVCRPWT 137
Db 124 KTKCGRGYKKGDEMGNTICKCKEKTYSYDVSDDQCKPMT 166

RESULT 23
Q911R5
ID Q911R5 PRELIMINARY; PRT; 186 AA.
AC Q911R5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumour necrosis family receptor.
GN A53R.
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USSR;
RA Reading P.C., Khanna A., Smith G.L.;
RT "Vaccinia virus encodes a soluble and cell surface tumour necrosis
RT factor receptor that contributes to viral virulence.";
RL Virology 0:0-0(0).
DR EMBL; AJ416893; CAC95181.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.

Query Match 11.8%; Score 169; DB 12; Length 186;
Best Local Similarity 31.3%; Pred. No. 2.9e-09;
Matches 42; Conservative 21; Mismatches 49; Indels 22; Gaps 8;

QY 28 CDNCQPGTFCR-----KYNPVCKSCPPSTFSSIGGQPN-CNICRVG-AGYFRFKFCSST 80
Db 51 CNCRPFGEFAKVRGNDNTKRCRCPHTYTAIPNYSNGCHQCRKCTGSPD-KVKCTGT 109
QY 81 HNAECICIGFHL--GPOCTCEKDCRQGE-----LTKQG--CKTCSLGTENDQ 127
Db 110 QNSKCSCLPGWCATDSSQTEDC-RDCIFKRRCPGCGYFGIDEQGNPICKSCCVSEYCDY 168
QY 128 NGTGVCVRPWTNCSL 141
Db 169 LRNYRLDPFPCKL 182

RESULT 24
Q9WJB4
ID Q9WJB4 PRELIMINARY; PRT; 186 AA.
AC Q9WJB4
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumour necrosis factor receptor precursor.
GN A53R.
OS Vaccinia virus (strain Lister).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10252;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lister;
RX MEDLINE=99226947; PubMed=10211965;
RA Alami A., Khanna A., Paul N., Smith J.L.;
RT "Vaccinia virus strains Lister, USSR and Evans express soluble and
RT cell-surface tumour necrosis factor receptors.";
RL J. Gen. Virol. 80:949-959(1999).
DR EMBL; Y17728; CAB41042.1; -.
DR HSP; Q92956; LUNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR Receptor; Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 186 AA; 20646 MW; D83CD9180276EE31 CRC64;

Query Match 11.8%; Score 169; DB 12; Length 186;
Best Local Similarity 31.3%; Pred. No. 2.9e-09;
Matches 42; Conservative 21; Mismatches 49; Indels 22; Gaps 8;

QY 28 CDNCQPGTFCR-----KYNPVCKSCPPSTFSSIGGQPN-CNICRVG-AGYFRFKFCSST 80
Db 51 CNCRPFGEFAKVRGNDNTKRCRCPHTYTAIPNYSNGCHQCRKCTGSPD-KVKCTGT 109

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DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 186 AA; 20662 MW; EF73D6A336A70C5A CRC64;

Query Match 11.8%; Score 169; DB 12; Length 186;
Best Local Similarity 31.3%; Pred. No. 2.9e-09;
Matches 42; Conservative 21; Mismatches 49; Indels 22; Gaps 8;

QY 28 CDNCQPGTFCR-----KYNPVCKSCPPSTFSSIGGQPN-CNICRVG-AGYFRFKFCSST 80
Db 51 CNCRPFGEFAKVRGNDNTKRCRCPHTYTAIPNYSNGCHQCRKCTGSPD-KVKCTGT 109
QY 81 HNAECICIGFHL--GPOCTCEKDCRQGE-----LTKQG--CKTCSLGTENDQ 127
Db 110 QNSKCSCLPGWCATDSSQTEDC-RDCIFKRRCPGCGYFGIDEQGNPICKSCCVSEYCDY 168
QY 128 NGTGVCVRPWTNCSL 141
Db 169 LRNYRLDPFPCKL 182

RESULT 24
Q9WJB4
ID Q9WJB4 PRELIMINARY; PRT; 186 AA.
AC Q9WJB4
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumour necrosis factor receptor precursor.
GN A53R.
OS Vaccinia virus (strain Lister).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10252;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lister;
RX MEDLINE=99226947; PubMed=10211965;
RA Alami A., Khanna A., Paul N., Smith J.L.;
RT "Vaccinia virus strains Lister, USSR and Evans express soluble and
RT cell-surface tumour necrosis factor receptors.";
RL J. Gen. Virol. 80:949-959(1999).
DR EMBL; Y17728; CAB41042.1; -.
DR HSP; Q92956; LUNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR Receptor; Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 186 AA; 20646 MW; D83CD9180276EE31 CRC64;

Query Match 11.8%; Score 169; DB 12; Length 186;
Best Local Similarity 31.3%; Pred. No. 2.9e-09;
Matches 42; Conservative 21; Mismatches 49; Indels 22; Gaps 8;

QY 28 CDNCQPGTFCR-----KYNPVCKSCPPSTFSSIGGQPN-CNICRVG-AGYFRFKFCSST 80
Db 51 CNCRPFGEFAKVRGNDNTKRCRCPHTYTAIPNYSNGCHQCRKCTGSPD-KVKCTGT 109

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QY 81 HNAECIEGPHCL--GQCTRCCKDCRPGQE-----LTKOG-----CKTCSLGTNDQ 127
Db 110 QNSKCSCLFGWYCATDSSQTEDC-RDCIPKRCPCGFGGIDEGNPICKSCCVGEYCDY 168
QY 128 NGTGVCRPWTNCSL 141
Db 169 LRNYRLDPFPCKL 182

RESULT 25.
O72735 PRELIMINARY; PRT; 186 AA.
AC O72735;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE A56R protein.
GN A56R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GRI-90.
RX MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutarov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RT smallpox, and vaccinia viruses.";
RL Virology 243:432-460(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=GRI-90.
RX MEDLINE=97068532; PubMed=8963248;
RA Saifonov P.F., Petrov N.A., Ryazankina O.I., Totmenin A.V.,
RA Shchelkunov S.N., Sandakhchiev L.S.;
RT "Genes of a circle of hosts for the cowpox virus.";
RL Dokl. Akad. Nauk 349:829-833(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=GRI-90;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Miheev M.V.,
RA Ryazankina O.I., Petrov N.A., Gutarov V.V., Kotwal G.J.,
RA Sandakhchiev L.S.;
RT "Structure-function and organization of cowpox virus strain GRI-90
RT complete genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=GRI-90;
RA Totmenin A.V.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94355; CAD90723.1; -.
DR HSSP; Q92956; 1JWA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;

Query Match 11.8%; Score 168; DB 12; Length 186;
Best Local Similarity 31.3%; Pred. No. 3.7e-09;
Matches 42; Conservative 20; Mismatches 50; Indels 22; Gaps 8;

QY 28 CDNCGFGTFCR-----KYNPVCKSPPTFFSISGQPN-CNICRVC-AGYFRFKFCST 80
Db 51 CNOCPFGFAKVRCSGSDTKRCRPHYTAIPNSGCHQCKRCKPTGSFD-KVCKTGT 109
QY 81 HNAECIEGPHCL--GQCTRCCKDCRPGQE-----LTKOG-----CKTCSLGTNDQ 127

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Db 110 QNSKCSCLFGWYCATDSSQTEDC-RDCVPKRCPCGFGGIDEGNPICKSCCVGEYCDY 168
QY 128 NGTGVCRPWTNCSL 141
Db 169 LRNYRLDPFPCKL 182

RESULT 26
O80YS6 PRELIMINARY; PRT; 285 AA.
AC O80YS6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE TNF decoy receptor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT fragments containing AU-rich elements.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401631; AAK91758.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR_3; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31795 MW; 5E3BD1B6EFC6BABC CRC64;

Query Match 11.8%; Score 168; DB 13; Length 285;
Best Local Similarity 26.2%; Pred. No. 5.8e-09;
Matches 58; Conservative 27; Mismatches 90; Indels 46; Gaps 12;

QY 4 NCYNVWVILLVGCCKVGVQVN-----SCDNCQFGTFCRKY-----NPVC 44
Db 6 NCFLLPLLVFALCGGVPVSGAHTPTIWRDDATGDSLTCDLCAPTVLLKHCTKDRKSDC 65
QY 45 KSCPSTFSSISGQ-PNCNIC-RVCAGYFRFKFCSTHNAECIEGPHCLGQCTRC 102
Db 66 GPCPKSHYTEIWNVIERCQCNRECTADEIESVPCTQLHNRQCECKDGFYTHGCSR-H 124
QY 103 KDCRPGQELTKQG-----CKTCSLGTND-NGTGVCRPWTNCSLDGRSLVLTGTTEK 154
Db 125 RRCPPGEGVINGTAHTDVKCEPCVGFSAVSSRRKACQKFSVCP-PGRTTI-PGNDMN 182
QY 155 DVVCGPPVWSPSTTISVTPGCGP--GGH-----SLOVLT 188
Db 183 DVYC-----SACRNGSRTHGOAICDGMELMFLSLQILT 216

RESULT 27
O8SQ34 PRELIMINARY; PRT; 278 AA.
AC O8SQ34;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CD40.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

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[illegible]

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RC STRAIN=Brighton Red;
RA Pickup D.J.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U55052; AAD10325.1; -.
DR EMBL; AF482758; AAM13631.1; -.
DR HSSP; Q92956; 1JMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
KW RECEPTOR.
SQ SEQUENCE 186 AA; 20372 MW; FC720DA743F62A2A CRC64;

Query Match 11.4%; Score 163; DB 12; Length 186;
Best Local Similarity 29.9%; Pred. No. 1.2e-08;
Matches 40; Conservative 21; Mismatches 51; Indels 22; Gaps 7;

QY 28 CDNCQPGTFCR-----KYNPVCKSCPPSTFFSIGGQFN-CNICRVC-AGYFRFKFCST 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 51 CNRCPEGFAKIRCSGSDNTKCRCPHTVTTVPNYSNGCHQCKPTGSGFD-KVKCTGT 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 81 HNAECIEGPHGLGQCTRC--KDCRPGQ-----ELTKGCKTCSLGTFFNDQ 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 110 QNSKSCSLPGWFC-ATDSSKTECDRCIPKRCQCGYFGGIDELGNPLCKSCCVGYCDD 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 NGTVGCRPWTNCSL 141
DB 169 IRNRVGPFPFCKL 182

RESULT 30
Q9PRG7 PRELIMINARY; PRT; 401 AA.
AC Q9PRG7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P75 neurotrophin receptor A-2.
GN P75NTRA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hutson L.D., Richards A.P., Bothwell M.;
RT "Life and death in the developing Xenopus retina: The role of the p75
RT neurotrophin receptor.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172400; AAD51031.1; -.
DR EMBL; AF172399; AAD51030.1; -.
DR HSSP; P07174; 1NGR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.

KW Receptor.
SQ SEQUENCE 401 AA; 43419 MW; D13BCAF7863EFECF CRC64;

Query Match 11.3%; Score 161.5; DB 13; Length 401;
Best Local Similarity 22.9%; Pred. No. 3.9e-08;
Matches 67; Conservative 37; Mismatches 102; Indels 87; Gaps 15;

QY 12 VLLLVGCEKVGAVQNS-----CDNCPQG-----TFCKYNPVCKSCPPS-TFS 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 5 LFIILGWAMLNAGKPCWNGSQYTAKECCISQVGGVIGKRCGVNQTVCPCLDSTVYS 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 54 -SIGGQNCNICRVACAGYFRFKFCSTTHNAECIEGPHC--LGPOCTCEKDCRGG-- 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 65 DTISHTACKPCTECFPGHKMEAPCVESDDAVACACAYGYFTDKSGGCKLC-KSCPFG 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 109 -----QELTKGCKTCSLGTFFNDQ-NGTGVCRPWTNCSLGDGRSVLKTGTTEKDVVC---G 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 MMSCTNIQDTICEKCEGYSDEDDNDPCLPCTICE-DGEIEAKCTFTSDTVCYDPN 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 PPVVSFGPS-----TTISVTPEG-----PGHSLQVLTILFALTALL 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 PRVSVTPASSDFPYTGTSTVPPFDLSSSSATSTGSKVLPFTGVAENLIPVYCSILA 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 LALI-FITLLFSLVKWIRKKPFHIFKQPFKKTGAQBEDACSCRCQEEEGG 250
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 243 AGLVAFIV-----FKWNS-----CKNQKGG 264
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 31
Q72762 PRELIMINARY; PRT; 167 AA.
AC Q72762
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE K3R protein.
GN K3R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90.
RX MEDLINE=98229462; PubMed=9568042;
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RT "Species-specific differences in genome organization of cowpox,
RT smallpox, and vaccinia viruses.";
RL Virology 243:432-460(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90.
RX MEDLINE=97068532; PubMed=8963248;
RA Saifonov P.F., Petrov N.A., Ryazankina O.I., Totmenin A.V.,
RA Shchelkunov S.N., Sandakhchiev L.S.;
RT "Genes of a circle of hosts for the cowpox virus.";
RL Dokl. Akad. Nauk 349:829-833(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Miheev M.V.,
RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,
RA Sandakhchiev L.S.;
RT "structure-function and organization of cowpox virus strain GRI-90
RT complete genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Totmenin A.V.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94355; CAD90751.1; -.

```


OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 RN NCBI_TaxID=9940;
 [1]
 RA Zwickowski M.S., Russ G.R., Krishnan R.;
 RP "Cloning and expression of the ovine CD40 molecule and the inhibition
 RT of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion
 RT protein.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RL ENBL; AY027298; AAL68402.1;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR008063; Fas receptor.
 DR Pfam; PF00020; TNFR C6.
 DR PRINTS; PR01680; PASRECEPTOR.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PSS0050; TNFR_NGFR_2; 1.
 FT NON TER 277
 SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;
 Query Match 10.9%; Score 155; DB 6; Length 277;
 Best Local Similarity 29.3%; Pred. No. 1.2e-07;
 Matches 44; Conservative 15; Mismatches 73; Indels 18; Gaps 7;
 QY 28 CDNCQPG---TFCRKYNPV-CKSCPPSTF-SSIGGFNPNICRVAGYFRFKFCSSTH 81
 DB 38 CDLCPPQKLLNDCTEVSKECTSCGKGEFLSTWREKYCHEHYRNPGLRIQSEGTL 97
 QY 82 NAE--CECIGFGLGPOCTRCED--CRPGQELTKG-----CKTCSLGTFF-NDQNG 129
 DB 98 NTDTTCVDCGQHCSTSTSCSPHSLCLFPGVKIATGVLTIQCEPVGFFSVSSA 157
 QY 130 TGVCRPWTNCSLDGRSVLKTGTTEKDVVCG 159
 DB 156 FERCHPWTSCERKGLVQHVGTNKTDAVCG 187
 QY 158 FERCHPWTSCERKGLVQHVGTNKTDAVCG 187
 ID Q7T2H3 PRELIMINARY; PRT; 318 AA.
 AC Q7T2H3;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Tumour necrosis factor receptor.
 GN TNFR.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 [1]
 RN TISSUE=Head kidney;
 RC Zou J., Seconbes C.J.;
 RA "Molecular cloning and expression analysis of a TNF receptor homologue
 RT in rainbow trout, Oncorhynchus mykiss.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ517804; CAD57165.1;
 SK Receptor.
 SQ SEQUENCE 318 AA; 35254 MW; 78F8135011283B43 CRC64;
 Query Match 10.8%; Score 154; DB 13; Length 318;
 Best Local Similarity 26.0%; Pred. No. 1.8e-07;
 Matches 40; Conservative 21; Mismatches 75; Indels 18; Gaps 6;
 QY 24 VQNSCDNCPGTFRC-----KYNFVKSCPPSTFSS-IGGFNPNICRVAGYFRFK--K 75

DB 18 VKRCRCRKGQVYRTDCKGKSTKTECQCQHEYYTABLNFKLQCLPCRVCVSSNQKVL 77
 QY 76 FCSSTHNAECIEGFCLGPOCTRC--EKDCRPGQELTKG-----CKTCSLGTFFND 126
 DB 78 ECEASSRQCCKTGYCTDGGCEHCLFVTLCLPGSGVNVQANPQNDTVCAPOPGTINS 137
 QY 127 QNGTGV-CRPWTNCSLDGRSVLKTGTTEKDVVCG 159
 DB 138 FNDFTQOSHTRCGDLGKEVKSAGTETTDVCG 171
 ID O57484 PRELIMINARY; PRT; 1792 AA.
 AC O57484;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Laminin beta 2-like chain.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93015947; PubMed=1400373;
 RX O'Rear J.J.;
 RA "A novel laminin B1 chain variant in avian eye.";
 RL J. Biol. Chem. 267:20555-20557(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98209634; PubMed=9550264;
 RX Liu J., Swadlow S., Xie W., Brewton R.G., Mayne R.;
 RA "Primary structure and expression of a chicken laminin beta chain:
 RT evidence for four beta chains in birds.";
 RL Matrix Biol. 16:471-481(1998).
 DR EMBL; AF038555; AAB92586.1; --
 DR HSP; P02468; IKLO.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR008211; LamNT.
 DR Pfam; PF00053; laminin_EGF; 13.
 DR Pfam; PF00055; laminin_Nterm; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR SMART; SM00180; EGF Lam; 13.
 DR SMART; SM00136; LamNT; 1.
 DR PROSITE; PS00022; EGF_1; 10.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 1792 AA; 195723 MW; 4A4CB0206F6A600 CRC64;
 Query Match 10.6%; Score 152; DB 13; Length 1792;
 Best Local Similarity 27.3%; Pred. No. 1.8e-06;
 Matches 67; Conservative 20; Mismatches 74; Indels 84; Gaps 17;
 QY 6 YNVVIVLLVCEKV-----GAVQNSCD-----NCQP-GTFRC-KYNPV--- 43
 DB 748 FHTVLSPPVAEPCSRLLHSLSLAILHNGALPCLDPQGSLSAECPQGGCCKPNVGR 807
 QY 44 CKSCPSTFSSIGGFNPNICRVAGYFRFKFCSSTHNAECIEGFCLGPOCTRC- 102
 DB 808 CHRCSPTGTF--GPRCDPCQ--CSGEGSLSAVC--DTVTGQCPQGAH--GSRCDRCOP 861
 QY 103 -----KDCRFGQ-----ELTKQCKTCSLGTFF-NDQNGTGV-GRP 135
 DB 862 GHWGFTFCPCQNGHABECDPQTGSLRCRDHTDGCRCQACAGHFGNPAALGSGQHCRP 921
 QY 136 W-----TNCSLDGRSVLKTGTTEKDVVCGPVPVSPSTTISVTPEGGPG-- 180

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Db 922 CPCPDGGRHFAASCYQGRS-----RQVVC-----HCSGYGTGPRCDRCAPGY 968
QY 181 GHSLQ 185
Db 969 GDPLO 973

RESULT 37
Q9JKE0 PRELIMINARY; PRT; 169 AA.
AC Q9JKE0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CD40 protein (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 62-169 FROM N.A.
RC STRAIN=wisar; TISSUE=Smooth muscle;
RX MEDLINE=99330195; PubMed=10403401;
RA Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
RT "Cytokine-inducible CD40 gene expression in vascular smooth muscle
RT cells is mediated by nuclear factor kappaB and signal transducer and
RT activator of transcription-1.";
RL FEBS Lett. 453:191-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=wisar; TISSUE=Smooth muscle;
RA Krzesz R., Hecker M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=wisar; TISSUE=Smooth muscle;
RA Gao D., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241231; AAF43717.2; -.
DR HSP; Q92956; 1JMA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004889; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007145; P:signal transduction; IEA.
DR InterPro; IPR008063; F:as receptor.
DR InterPro; IPR001865; Ribosomal S2.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
FT NON TER 169
SQ SEQUENCE 169 AA; 18525 MW; F199D91EFA224A26 CRC64;

Query Match 10.6%; Score 151; DB 11; Length 169;
Best Local Similarity 30.3%; Pred. No. 1.8e-07;
Matches 40; Conservative 17; Mismatches 53; Indels 22; Gaps 8;

QY 28 CDNCQPG---TFCKYKNV-CKSCPSTSSIGQP-NCNCRVCA--GYFRKPKFSS 79
Db 38 CDLCQGNRLVSHCTALEKTCQCDGSGSAHNREIRCHQHCNQLQVKKEGTA 97
QY 80 THNAECIEGFHCLGQCTFC--EKDCRG-----QELTKGCKTCSLGTFFNDQNGT 130
Db 98 VSDTVCTCKEGQHCASKECETCAQHRPCGPGVGIVQVQATTTDTVCQPCVPGFFS--NGS 155

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QY 131 GV---CRPWTNC 139
Db 156 SLFEKCHPWTSC 167

RESULT 38
Q8JFU6 PRELIMINARY; PRT; 235 AA.
AC Q8JFU6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S1:d294E17.1 (Novel protein similar to nerve growth factor receptor
DE (NGFR)) (fragment).
GN S1:D294E17.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL596203; CAD43457.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON TER 235
SQ SEQUENCE 235 AA; 25783 MW; 7C6CASFAB16E7BE CRC64;

Query Match 10.6%; Score 151; DB 13; Length 235;
Best Local Similarity 24.4%; Pred. No. 2.6e-07;
Matches 58; Conservative 35; Mismatches 85; Indels 60; Gaps 12;

QY 51 TFS-SIGGPNICRVKAGYPRFKKFCSTHNAECIEGF--HCLGQCTRCCKDRP 107
Db 2 TFSATFHTDKQVCTECTGLMRMQTPCTDSNDAECVNGYFMNVLSSRCEPCTV-CPL 60
QY 108 GO-----ELTKQG-CKTCSLGTFFNDQNGT-GVCRPWTNCSLDGRSVLTKGTTEKDVVG 159
Db 61 GGVDMRCNLNHDVTCECRDETYSQDNTMPCICTCEDTTEILLRNCPTTDEALCH 120
QY 160 PPVWSFSPSTTISVTPG-----GPG-----GHSLOVLTFL 191
Db 121 DFL---SPYPTSTGSGSFDLRLWSRPSGDDATTPKSPSPHFICRGLNENLPIYC 177
QY 192 ALTSALLALIFITLLFVLKWKIRKPHIPKQ--PFKTTGAQEEEDACRCRCPQEE 247
Db 178 SILAAVVGVL-----LAYI-----IFKRWNSCKQKQANNAATANQTPSPE 220

RESULT 39
Q8LRM7 PRELIMINARY; PRT; 1997 AA.
AC Q8LRM7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mastigoneme-like protein.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]

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RP SEQUENCE FROM N.A.
RA Song L., Dentler W.L.;
RT "Molecular cloning and characterization of a 240 kDa flagellar protein
in Chlamydomonas";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508983; AAM33652.1; -
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Peptidase S8.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
SQ SEQUENCE 1997 AA; 206459 MW; A4061C41FEAA7047 CRC64;
Query Match 10.5%; Score 149.5; DB 10; Length 1997;
Best Local Similarity 26.5%; Pred. No. 3.7e-06;
Matches 53; Conservative 24; Mismatches 64; Indels 59; Gaps 12;
QY 28 CDNCQPGTECRKYN-PVCKSCPPSTFSSIGGPNQCNICR-----VCA----- 68
DB 1603 CYTCQTGTDFEFQVPCACACWGSFASRGGLPTCEIAQPGTFNTVAANAATENTATLI 1662
QY 69 -----GYFRFKKFCSSSTHABC-ECIEGFHCLGPOCTCEKDCRPGQ-- 109
DB 1663 PTGLVKAQAQPTCGMGYFQ-----SSAETTTCTACAVGTADQAGLAAC-KPCOPGRYQ 1716
QY 110 -ELTKGCKTCSLGTNDQGTGVCPRPWNCSLDGRSVLKTGTETKDVVCGPPVVSF--- 165
DB 1717 NSIGQVCKPCDNGTYSRYGGE-LC---TKCPA-GTVASKTSSQ-----CTPCAAGFYAN 1767
QY 166 --SPSTTISVTPEGGPGGHS 183
DB 1768 APDSATSCRACPRGYGYPYS 1787
RESULT 40
Q8BZU6 Q8BZU6 PRELIMINARY; PRT; 573 AA.
AC Q8BZU6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Death receptor 6.
GN TNFRSP21 OR AA959878.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=23354683; Pubmed=12466851;
RA the FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK033529; BAC28342.1; -
DR MGI; MGI:2151075; Tnfrsf21.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
SQ SEQUENCE 573 AA; 63506 MW; BC883B4EC8F2FE94 CRC64;
Query Match 10.3%; Score 146.5; DB 11; Length 573;
Best Local Similarity 29.9%; Pred. No. 2e-06;
Matches 50; Conservative 18; Mismatches 64; Indels 35; Gaps 9;

QY 43 VKSCPPSTFS-SIGQPNQCNIC-RVCAGYFRFKKFCSSSTHNAECIEGFHCLGPGQCTR 100
DB 5 VCSSCPAGTTRHENGIERCHDCSPCPWMIERLLPCALTDRICCPGPMYQNGTCAP 64
QY 101 CEKDCRPGQELTKQG-----CKTCSLGTEND-QNGTGVCRPWNCSLDGRSVLKTGTT 152
DB 65 -HIVCPVGVGVYRKKGTENEDVRCKQCARGTFSDVPSSVMCKAHTDCLGQNLVVKPGTK 123
QY 153 EKDVCVG-----PP-----VVSFS-----PSTTISVTPEG 177
DB 124 ETDNVCGMRLFFSSTNPFSSGTVTFSHPHEHSHEDVFSPTYE--PQG 168
Search completed: May 5, 2004, 14:40:33
Job time : 89.6712 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:20 ; Search time 5.46233 Seconds
(without alignments)
568.992 Million cell updates/sec

Title: US-10-067-122B-2_COPY_105_115

Perfect score: 62
Sequence: 1 CRPGQLTKQG 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp1950s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	7	ADC25950 Murine re
2	62	100.0	191	4	AAB66986 41bb prot
3	62	100.0	256	2	AAR64199 Murine 4-
4	62	100.0	256	2	AAR70978 4-1BB rec
5	62	100.0	256	2	AAW04173 Mouse rec
6	62	100.0	256	2	AAW26659 Mouse 4-1
7	62	100.0	256	2	AAW26687 Mouse Rec
8	62	100.0	256	2	AAW28687 Murine CD
9	62	100.0	256	5	AAE22581 Mouse rec
10	62	100.0	256	5	ABB75954 Murine cy
11	62	100.0	256	7	ADC25939 Murine re
12	62	100.0	256	7	ADe87549 Mouse rec
13	57	91.9	12	5	AAE22582 Mouse rec
14	57	91.9	12	7	ADC25944 Murine re
15	50	80.6	255	2	AAR74087 Human rec
16	47	75.8	132	3	AAW94714 Tumour ne
17	47	75.8	219	2	AAW31759 A novel h
18	47	75.8	219	2	AAW92523 Human h4-
19	47	75.8	219	2	AAW92524 Human h4-
20	47	75.8	219	4	AAE08545 Human h4-
21	47	75.8	219	6	ABB84639 Human h4-
22	47	75.8	255	2	AAR64197 Human 4-1
23	47	75.8	255	2	AAR70977 H4-1BB re
24	47	75.8	255	2	AAW04174 Human rec
25	47	75.8	255	2	AAW26658 Human 4-1

26	47	75.8	255	2	AAW28688 Human rec
27	47	75.8	255	2	AAW33214 Human CD1
28	47	75.8	255	4	AAB08546 Human h4-
29	47	75.8	255	4	AAB50521 Human tum
30	47	75.8	255	5	ABW75955 Human cyt
31	47	75.8	255	6	ABR39863 Human MOC
32	47	75.8	255	6	ABB84640 Human h4-
33	47	75.8	255	7	AAE39531 Human pro
34	47	75.8	255	7	ADC78803 Human PRO
35	47	75.8	255	7	Add25599 Binding d
36	47	75.8	255	7	ADe87541 Unknown h
37	43	69.4	265	6	AAE29933 Human LP2
38	43	69.4	389	4	AAU02951 Angiogens
39	43	69.4	845	5	AAW68259 Human POL
40	43	69.4	845	6	ABU12092 Novel hum
41	43	69.4	845	7	AAE38807 Human POL
42	43	69.4	880	7	ADb64680 Human pro
43	43	69.4	897	4	AAE65887 Amino aci
44	43	69.4	897	4	ABG06309 Novel hum
45	43	69.4	897	5	ABG91402 Primate L

ALIGNMENTS

RESULT 1
ADC25950
ID ADC25950 standard; peptide; 11 AA.

XX AC ADC25950;

XX DT 18-DEC-2003 (first entry)

XX DE Murine receptor 4-1BB peptide - residues 105-115.

XX KW receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation; cancer; murine; mouse.

XX OS Mus musculus.

XX PN US2003100745-A1.

XX PD 29-MAY-2003.

XX PF 04-FEB-2002; 2002US-00067122.

XX PR 07-NOV-1988; 88US-00267577.

XX PR 30-JUL-1992; 92US-00922996.

XX PR 01-FEB-1993; 93US-00012269.

XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX Kwon BS;

XX WPI; 2003-678138/64.

XX New cDNA gene encoding receptor protein 4-1BB, useful for isolating similar DNA sequences, and the encoded polypeptide and an antibody to it, useful for identifying ligands, and for modulating immune cell activity.

XX Disclosure; Page 22; 77pp; English.

XX The invention relates to a novel cDNA gene encoding receptor protein 4-1BB. The cDNA gene of the invention demonstrates immunostimulant activities and may be useful as a probe to isolate DNA sequences encoding for proteins similar to the receptor protein encoded by the DNA. The protein, its fragments and derivatives may be useful as a probe to isolate ligands to receptor protein 4-1BB, for stimulating proliferation of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand binding. The antibody may be useful for enhancing T-cell proliferation or activation. Finally, the invention may be useful with respect to cancer research. The current sequence is that of the murine receptor 4-1BB peptide (residues 105-115) of the invention.

XX SQ Sequence 11 AA;
 Query Match 100.0%; Score 62; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0003;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 |||||
 Db 1 CRPGQELTKQG 11
 |||||
 RESULT 2
 AAB66986
 ID AAB66986 standard; protein; 191 AA.
 XX
 AC AAB66986;
 DT 19-APR-2001 (first entry)
 XX
 DE 41bb protein.
 XX
 KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
 KW ischaemia; Parkinson's disease.
 XX
 OS Unidentified.
 XX
 PN WO200103719-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 07-JUL-2000; 2000WO-US018667.
 XX
 PR 09-JUL-1999; 99US-00350670.
 PR 09-DEC-1999; 99US-00457647.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
 XX
 DR WPI; 2001-103031/11.
 XX
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
 PT protein in conjunction with e.g. inhibitors of interleukin and tumor
 PT necrosis factor alpha.
 XX
 PS Disclosure; Fig 2; 316pp; English.
 XX
 CC The present invention relates to a method for treating conditions leading
 CC to bone loss. The method comprises administering a purified and isolated
 CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
 CC in conjunction with other substances such as tumour necrosis factor-alpha
 CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
 CC modulators, fibroblast growth factor (FGF)-10 modulators and/or platelet
 CC activating factor (PAF) antagonists. The method is useful for treating
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
 CC graft-versus-host disease (GVHD). Other diseases that can be treated
 CC include acute pancreatitis, Alzheimer's disease, anorexia,
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock. The present sequence was used in a sequence
 CC homology comparison
 XX
 SQ Sequence 191 AA;
 Query Match 100.0%; Score 62; DB 4; Length 191;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 |||||
 Db 105 CRPGQELTKQG 115
 |||||
 RESULT 3
 AAR64199
 ID AAR64199 standard; protein; 256 AA.
 XX
 AC AAR64199;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-AUG-1995 (first entry)
 XX
 DE Murine 4-1BB polypeptide.
 XX
 KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
 KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
 XX
 OS Mus musculus.
 XX
 PN WO9426290-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 06-MAY-1994; 94WO-US005036.
 XX
 PR 07-MAY-1993; 93US-00060843.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Goodwin RG, Smith CA, Alderson MR;
 XX
 DR WPI; 1995-022265/03.
 DR N-PSDB; AAQ75428.
 XX
 PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB
 PT to transduce signal.
 XX
 PS Example 1; Page 44-45; 65pp; English.
 XX
 CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75422)
 CC are useful in a pharmaceutical composition for stimulating the immune
 CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring
 CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.
 CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation
 CC of primary T-cells during the derivation of clonal T-cell lines. It may
 CC also be used to stimulate proliferation of activated T-cells, used in
 CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 256 AA;
 Query Match 100.0%; Score 62; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 |||||
 Db 105 CRPGQELTKQG 115
 |||||
 RESULT 4
 AAR70978
 ID AAR70978 standard; protein; 256 AA.
 XX
 AC AAR70978;
 XX
 DT 25-MAR-2003 (revised)

DT 16-OCT-1995 (first entry)
 XX 4-1BB receptor protein.
 DE 4-1BB; receptor protein; immunosuppressive; autoimmune disease;
 XX organ transplantation; cell membrane ligand.
 KW Mus sp.
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Sig_peptide
 XX WO9507984-A1.
 PN 23-MAR-1995.
 XX 15-SEP-1994; 94WO-US010457.
 PF 16-SEP-1993; 93US-00122796.
 PR (INDV) UNIV INDIANA FOUND.
 XX Kwon BS;
 PI WPI; 1995-131352/17.
 DR N-PSDB; AAQ86127.
 XX Novel cDNA encoding human receptor protein H4-1BB - useful to produce the
 PT protein which is used to treat autoimmune disease and facilitate organ
 PT transplantation.
 XX Disclosure; Fig 1; 36pp; English.
 PS cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was
 CC isolated using PCR primers based on the homologous mouse 4-1BB gene
 CC (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR
 CC -2003 to correct PN field.)
 XX Sequence 256 AA;
 SQ Query Match 100.0%; Score 62; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 DB 105 CRPGQELTKQG 115
 RESULT 5
 AAW04173
 ID AAW04173 standard; protein; 256 AA.
 XX AC AAW04173;
 XX 12-DEC-1996 (first entry)
 DT Mouse receptor 4-1BB.
 DE Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
 XX immunostimulant; cancer; autoimmune disease; graft rejection; therapy.
 KW Mus sp.
 XX WO9629348-A1.
 PN 26-SEP-1996.
 XX 22-MAR-1996; 96WO-US003965.
 PF 23-MAR-1995; 95US-00409851.
 PR (INDV) UNIV INDIANA FOUND.
 XX Kwon BS;
 PI WPI; 1996-443138/44.
 DR N-PSDB; AAT39541.
 XX Monoclonal antibody specific for human receptor protein 4-1BB - used to
 PT enhance proliferation and activation of T-cells for treatment of cancer
 PT and to inhibit specific ligand binding for treating autoimmune diseases.
 XX Disclosure; Page 32-34; 48pp; English.
 XX Novel murine receptor protein 4-1BB (AAW04173) has the potential to
 CC function as an accessory signaling molecule during T-cell activation and
 CC proliferation. It may represent a cell surface molecule involved in T-
 CC cell-APC interactions and may also act as a B-cell costimulator. It is
 CC structurally related to members of the nerve growth factor receptor
 CC superfamily. Its amino acid sequence was deduced from an isolated cDNA
 CC clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was
 CC identified and used to raise a monoclonal antibody useful in cancer and
 CC autoimmune disease therapy
 XX Sequence 256 AA;
 SQ Query Match 100.0%; Score 62; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 DB 105 CRPGQELTKQG 115
 RESULT 6
 AAW26659
 ID AAW26659 standard; protein; 256 AA.
 XX AC AAW26659;
 XX 25-MAR-2003 (revised)
 DT 25-FEB-1998 (first entry)
 XX Mouse 4-1BB receptor.
 DE 4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell;
 XX proliferation; immunostimulant.
 KW Mus musculus.
 XX OS
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Sig_peptide
 XX US5674704-A.
 PN 07-OCT-1997.
 PD 06-MAY-1994; 94US-00236918.
 XX 07-MAY-1993; 93US-00060843.
 PR (IMMV) IMMUNEX CORP.
 XX Alderson MR, Goodwin RG, Smith CA;
 PI WPI; 1997-502333/46.
 DR N-PSDB; AAT91027.
 XX DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell
 PT proliferation in vitro, and as research tools.
 XX Disclosure; Col 39-40; 32pp; English.
 PS

PA (INDV) UNIV INDIANA FOUND.
 XX Kwon BS, Kang C;
 XX WPI; 1996-443138/44.
 DR N-PSDB; AAT39541.
 XX Monoclonal antibody specific for human receptor protein 4-1BB - used to
 PT enhance proliferation and activation of T-cells for treatment of cancer
 PT and to inhibit specific ligand binding for treating autoimmune diseases.
 XX Disclosure; Page 32-34; 48pp; English.
 XX Novel murine receptor protein 4-1BB (AAW04173) has the potential to
 CC function as an accessory signaling molecule during T-cell activation and
 CC proliferation. It may represent a cell surface molecule involved in T-
 CC cell-APC interactions and may also act as a B-cell costimulator. It is
 CC structurally related to members of the nerve growth factor receptor
 CC superfamily. Its amino acid sequence was deduced from an isolated cDNA
 CC clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was
 CC identified and used to raise a monoclonal antibody useful in cancer and
 CC autoimmune disease therapy
 XX Sequence 256 AA;
 SQ Query Match 100.0%; Score 62; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 DB 105 CRPGQELTKQG 115
 RESULT 6
 AAW26659
 ID AAW26659 standard; protein; 256 AA.
 XX AC AAW26659;
 XX 25-MAR-2003 (revised)
 DT 25-FEB-1998 (first entry)
 XX Mouse 4-1BB receptor.
 DE 4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell;
 XX proliferation; immunostimulant.
 KW Mus musculus.
 XX OS
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Sig_peptide
 XX US5674704-A.
 PN 07-OCT-1997.
 PD 06-MAY-1994; 94US-00236918.
 XX 07-MAY-1993; 93US-00060843.
 PR (IMMV) IMMUNEX CORP.
 XX Alderson MR, Goodwin RG, Smith CA;
 PI WPI; 1997-502333/46.
 DR N-PSDB; AAT91027.
 XX DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell
 PT proliferation in vitro, and as research tools.
 XX Disclosure; Col 39-40; 32pp; English.
 PS

XX This protein comprises mouse 4-1BB, a member of the tumour necrosis
 CC factor receptor superfamily that is expressed on helper, suppressor and
 CC cytolytic T cells, as well as on mouse brain tissue. A novel claimed
 CC cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned
 CC and sequenced (see AAM26656) that binds to murine 4-1BB. 4-1BB-L,
 CC especially its soluble extracellular domain, can be used to stimulate T-
 CC cell proliferation in vitro, as a research tool and as an affinity ligand
 CC for purifying 4-1BB. (Updated on 25-MAR-2003 to correct Pf field.)
 XX
 SQ Sequence 256 AA;

Query Match 100.0%; Score 62; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11
 Db 105 CRPQELTKQG 115

RESULT 7
 AAY28687
 ID AAY28687 standard; protein; 256 AA.

AC AAY28687;

DT 13-OCT-1999 (first entry)

DE Mouse Receptor 4-1BB protein.

KW Mouse Receptor 4-1BB cDNA; Mouse Receptor 4-1BB protein; H4-1BB protein;
 KW human 4-1BB protein; T cell activation; proliferation; immune response;
 KW receptor protein; autoimmune disease; organ transplantation;
 KW cancerous tumour; nerve growth factor receptor.

OS Mus musculus.

FN WO9936093-A1.

PD 22-JUL-1999.

PF 14-JAN-1999; 99WO-US000823.

PR 14-JAN-1998; 98US-00007097.

PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

PA (KWON/) KWON B S.

PI Kwon BS;

DR WPI; 1999-444325/37.

DR N-FSDB; AAX90763.

PT Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
 PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.

PS Disclosure; Page 75; 86pp; English.

XX The present sequence is mouse 4-1BB receptor protein. This protein has
 CC 65% homology with human receptor protein 4-1BB. The protein has a
 CC putative leader sequence, a potential membrane anchor segment and other
 CC features of known receptor proteins. 4-1BB is structurally related to
 CC members of the nerve growth factor receptor. Probes derived from mouse 4-
 CC 1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its
 CC ligands, and various monoclonal antibodies have therapeutic uses. They
 CC may be used to enhance or suppress T cell activation and proliferation;
 CC for activation or inhibition of immune response; to block H4-1BB ligand
 CC binding; treating cancerous tumours and autoimmune diseases; and during
 CC organ transplantation

XX Sequence 256 AA;

Query Match 100.0%; Score 62; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11
 Db 105 CRPQELTKQG 115

RESULT 8
 AAY33215
 ID AAY33215 standard; protein; 256 AA.

AC AAY33215;

DT 18-NOV-1999 (first entry)

DE Murine CD137 protein.

KW CD137; monocyte growth factor; proliferation; peripheral monocyte;
 KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;
 KW immunostimulatory; non-specific immune response; phagocytosis;
 KW intracellular destruction; microorganism; immune complex; antibody;
 KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
 KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
 KW bacterial; viral infection; immunosuppressant; gene therapy; murine.

OS Mus sp.

FN WO9944629-A2.

PD 10-SEP-1999.

PF 05-MAR-1999; 99WO-EP001440.

PR 05-MAR-1998; 98EP-00103859.

PA (MERC) MERCKLE GMBH.

PI Schwarz H, Langstein J;

DR WPI; 1999-550983/46.

PT Use of monocyte growth factor CD137 for stimulating proliferation of
 PT peripheral monocytes, particularly for treating immune deficiency, e.g.
 PT following cancer therapy.

PS Disclosure; Fig 1B; 57pp; German.

XX This invention describes a novel use of the human monocyte growth factor
 CC CD137, or its functional analogs, for (i) stimulating proliferation of
 CC peripheral monocytes; and (ii) treating diseases that are associated with
 CC disorders of a cellular system that includes monocytes (and/or their
 CC derived cells, precursor or progenitors) or where the origin and/or
 CC progression is treatable by stimulating proliferation of such cells. The
 CC products of the invention have antitumor, antibacterial, antiviral,
 CC antifungal and immunostimulatory activity. Stimulating proliferation of
 CC monocytes promotes the non-specific immune response, i.e. it increases
 CC phagocytosis and intracellular destruction of microorganisms, immune
 CC complexes and damaged cells, and improves antibody (in)dependent
 CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
 CC diseases associated with a defective immune response where caused by
 CC inadequate numbers of active monocytes/macrophages, especially damage to
 CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation
 CC therapy; disorders of wound healing (e.g. in dialysis or diabetic
 CC patients, or those with chronic venous insufficiency); tumors; bacterial,
 CC fungal or viral infections; (non-)congenital or (non-)inherited diseases
 CC or injury to the immune system; injury induced by treatment with
 CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune
 CC disease, or transplant patients). Nucleic acid encoding (I) can be used
 CC similarly, in gene therapy procedures. Proliferation of peripheral
 CC monocytes is achieved independently of hematopoietic stem cells. This
 CC sequence represents the murine CD137 protein described in the method of

ID ADC25939 standard; protein; 256 AA.
 XX AC ADC25939;
 XX DT 18-DEC-2003 (first entry)
 XX DE Murine receptor 4-1BB protein.
 XX KW receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;
 XX KW cancer; murine; mouse.
 XX OS Mus musculus.
 XX PN US2003100745-A1.
 XX PD 29-MAY-2003.
 XX PF 04-FEB-2002; 2002US-00067122.
 XX PR 07-NOV-1988; 88US-00267577.
 XX PR 30-JUL-1992; 92US-00922996.
 XX PR 01-FEB-1993; 93US-00012269.
 XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
 XX PA Kwon BS;
 XX PI WPI; 2003-678138/64.
 XX DR N-PSDB; ADC25938.
 XX New CDNA gene encoding receptor protein 4-1BB, useful for isolating
 PT similar DNA sequences, and the encoded polypeptide and an antibody to it,
 PT useful for identifying ligands, and for modulating immune cell activity.
 XX Claim 7; Fig 2; 77pp; English.
 XX The invention relates to a novel CDNA gene encoding receptor protein 4-
 CC 1BB. The CDNA gene of the invention demonstrates immunostimulant
 CC activities and may be useful as a probe to isolate DNA sequences encoding
 CC for proteins similar to the receptor protein encoded by the DNA. The
 CC protein, its fragments and derivatives may be useful as a probe to
 CC isolate ligands to receptor protein 4-1BB, for stimulating proliferation
 CC of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand
 CC binding. The antibody may be useful for enhancing T-cell proliferation or
 CC activation. Finally, the invention may be useful with respect to cancer
 CC research. The current sequence is that of the murine receptor 4-1BB
 CC protein of the invention.
 XX SQ Sequence 256 AA;
 Query Match 100.0%; Score 62; DB 7; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 DB 105 CRPGQELTKQG 115
 RESULT 12
 ADE87549
 ID ADE87549 standard; protein; 256 AA.
 XX AC ADE87549;
 XX DT 29-JAN-2004 (first entry)
 XX DE Mouse receptor H4-1BB.
 XX KW immunosuppressive; H4-1BB ligand binding blocker; mouse;
 KW receptor protein; H4-1BB; B-cell proliferation stimulator;
 KW T-cell proliferation enhancer; immune system suppressor; transplantation;
 KW autoimmune disease.

XX Mus sp.
 OS US2003082157-A1.
 PN 01-MAY-2003.
 PD 12-JUN-2002; 2002US-00170997.
 PF 07-NOV-1988; 88US-00267577.
 PR 30-JUL-1992; 92US-00922996.
 PR 01-FEB-1993; 93US-00012269.
 PR 05-JUN-1995; 95US-00460976.
 PR 22-OCT-1997; 97US-00955573.
 XX (KWON/) KWON B S.
 XX Kwon BS;
 XX WPI; 2003-576599/54.
 XX DR N-PSDB; ADE87548.
 XX New CDNA, or its encoded receptor protein H4-1BB, useful as probes to
 PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking
 PT H4-1BB ligand binding to facilitate organ transplantation or treat
 PT autoimmune diseases.
 XX Disclosure; Fig 1; 19pp; English.
 XX The invention describes a CDNA, which encodes for human receptor protein
 CC H4-1BB. The CDNA, or its fragments or derivatives, are useful as a probe
 CC to isolate DNA sequences encoding for proteins similar to the receptor
 CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or
 CC derivatives, is useful as a probe for identifying ligands to the receptor
 CC protein H4-1BB, or for stimulating the proliferation of B-cells
 CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are
 CC useful for enhancing T-cell proliferation of activation. The CDNA or
 CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand
 CC binding, which is particularly useful for suppressing the immune system
 CC during transplantation, or for treating autoimmune diseases. This is the
 CC amino acid sequence of mouse receptor H4-1BB.
 XX SQ Sequence 256 AA;
 Query Match 100.0%; Score 62; DB 7; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 DB 105 CRPGQELTKQG 115
 RESULT 13
 AAE22582
 ID AAE22582 standard; peptide; 12 AA.
 XX AC AAE22582;
 XX DT 26-JUL-2002 (first entry)
 XX DE Mouse receptor 4-1BB peptide.
 XX KW Mouse; lymphokine; L2G25B; macrophage inflammatory protein 1 alpha;
 KW MIP-1alpha; immune disease; myeloid progenitor cell differentiation;
 KW 4-1BB; receptor.
 XX OS Mus sp.
 XX US6355476-B1.
 XX PD 12-MAR-2002.
 XX

30-JUL-1992; 92US-00922996.
 07-NOV-1988; 88US-00267577.
 (ADRE-) ADVANCED RES & TECHNOLOGY INC.
 Kwon BS, Broxmeyer HB;
 WPI; 2002-370577/40.
 New isolated and purified cDNA designated L25G25B encoding the mouse lymphokine macrophage inflammatory protein 1 alpha which can be used for modulating early myeloid progenitor cell differentiation.
 Disclosure; Col 53; 8pp; English.
 The invention relates to an isolated and purified cDNA containing mouse lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by which the immune cells communicate with each other. Lymphokines are used therapeutically against immunologic diseases. Mouse lymphokine MIP-1alpha can be used to modulate early myeloid progenitor cell differentiation.
 The present sequence is mouse lymphokine receptor 4-1BB peptide

Sequence 12 AA;
 Query Match 91.9%; Score 57; DB 5; Length 12;
 Best Local Similarity 90.9%; Pred. No. 0.0026;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 |||||
 Db 1 CRPGQELTKSG 11
 |||||

RESULT 14
 ADC25944
 ID ADC25944 standard; peptide; 12 AA.
 AC ADC25944;
 DT 18-DEC-2003 (first entry)
 DE Murine receptor 4-1BB peptide containing residues 105-115.
 KW receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;
 KW cancer; murine; mouse.
 OS Synthetic.
 OS Mus musculus.
 PN US2003100745-A1.
 PD 29-MAY-2003.
 PF 04-FEB-2002; 2002US-00067122.
 PR 07-NOV-1988; 88US-00267577.
 PR 30-JUL-1992; 92US-00922996.
 PR 01-FEB-1993; 93US-00012269.
 PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
 PI Kwon BS;
 PI WPI; 2003-678138/64.
 DR New cDNA gene encoding receptor protein 4-1BB, useful for isolating
 PT similar DNA sequences, and the encoded polypeptide and an antibody to it,
 PT useful for identifying ligands, and for modulating immune cell activity.
 XX Disclosure; Page 14; 77pp; English.

The invention relates to a novel cDNA gene encoding receptor protein 4-1BB. The cDNA gene of the invention demonstrates immunostimulant activities and may be useful as a probe to isolate DNA sequences encoding for proteins similar to the receptor protein encoded by the DNA. The protein, its fragments and derivatives may be useful as a probe to isolate ligands to receptor protein 4-1BB, for stimulating proliferation of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand binding. The antibody may be useful for enhancing T-cell proliferation or activation. Finally, the invention may be useful with respect to cancer research. The current sequence is that of the murine receptor 4-1BB peptide of the invention which contains residues 105-115.

Sequence 12 AA;
 Query Match 91.9%; Score 57; DB 7; Length 12;
 Best Local Similarity 90.9%; Pred. No. 0.0026;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 |||||
 Db 1 CRPGQELTKSG 11
 |||||

RESULT 15
 AAR74087
 ID AAR74087 standard; protein; 255 AA.
 AC AAR74087;
 DT 21-JAN-1996 (first entry)
 DE Human receptor induced by lymphocyte activation (ILA).
 KW ILA; receptor inducible by lymphocyte activation; disease diagnosis;
 KW antiinflammatory.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..17
 FT /note= "signal peptide"
 FT Misc-difference 138
 FT /note= "potential N-glycosylation site"
 FT Misc-difference 149
 FT /note= "potential N-glycosylation site"
 FT Domain 187..213
 FT /note= "transmembrane domain"
 FT Misc-difference 234
 FT /note= "casein-kinase-II phosphorylation site"
 FT Misc-difference 235
 FT /note= "casein-kinase-II phosphorylation site"
 FT Binding-site 241..244
 FT /note= "potential ligand binding site"
 FT Misc-difference 242
 FT /note= "protein-kinase phosphorylation site"
 PN CA2108401-A.
 XX 28-MAR-1995.
 XX 14-OCT-1993; 93CA-02108401.
 XX 27-SEP-1993; 93US-00127693.
 XX (REGC) UNIV CALIFORNIA.
 XX Lotz M, Schwarz H;
 XX WPI; 1995-194420/26.
 DR N-PSDB; AAR74087.
 XX New receptor inducible by lymphocyte activation - used to develop prods.
 PT for the diagnosis and treatment of inflammatory host defence pathology.

XX
PS
XX
XX
Claim 55; Page 61; 91pp; English.
XX
CC
XX
ILIA may be used to identify a host defence inflammatory response in body
tissue. The ILA agents can be used to detect an ILA-mediated pathology
CC
CC
such as atherosclerosis, autoimmune disease (rheumatoid arthritis,
CC
CC
transplant rejection, pathogenic host defense responses to microorganism
CC
CC
and malignancy such as lung carcinoma
XX
SQ
Sequence 255 AA;
Query Match 80.6%; Score 50; DB 2; Length 255;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPGQELTKQG 11
Db 106 CRQGQELTKKG 116
RESULT 16
AAV94714
ID AAY94714 standard; protein; 132 AA.
XX
AC AAY94714;
XX
XX
XX
29-JAN-2001 (first entry)
XX
DE Tumour necrosis factor receptor (TNFR) domain of 4-1BB protein.
XX
XX
XX
Tumour necrosis factor-related protein; TR2; human; cancer;
KW
Chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
KW
immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
KW
severely combined immunodeficiency; apoptosis inhibition;
KW
Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
OS Homo sapiens.
XX
XX
WO200056405-A2.
XX
XX
28-SEP-2000.
XX
XX
22-MAR-2000; 2000WO-US007521.
XX
XX
22-MAR-1999; 99US-0125683P.
XX
26-MAR-1999; 99US-0126522P.
XX
20-MAY-1999; 99US-0135169P.
XX
06-AUG-1999; 99US-0147383P.
XX
XX
(NIJ/) NI J.
PA
(ROSE/) ROSEN C A.
PA
(GENTZ/) GENTZ R L.
XX
XX
Ni J, Rosen CA, Gentz RL;
PI
WPI; 2000-594519/56.
DR
XX
XX
Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT
and its two splice variants, useful for treating arthritis or
PT
inflammation, cancer (such as follicular lymphomas) and immunodeficiency
PT
disorders.
XX
XX
Disclosure; Fig 16; 373pp; English.
XX
XX
XX
This invention relates to an isolated nucleic acid molecule encoding a
human tumor necrosis factor (TNF)-receptor related protein TR2. Included
in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC
CC
The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
member of the TNFR superfamily. The invention includes a method for the
CC
CC
treatment of arthritis or inflammation using an antibody directed against
a fragment of the TR2 protein. TR2 is an agonist, antagonists and
CC
CC
antibodies exhibit cytostatic, dermatological, antineoplastic,
immunosuppressive, anti-allergic, antiarthritic, antiasthmatic,

XX
CC
antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
cerebroprotective activity. The methods are useful for treating arthritis
or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
mutations, cardiac tumors, pancreatic, breast, or prostate cancer), an
immunodeficiency or for enhancing an in vivo leukocyte response to an
antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
inflammatory myopathies) and immunodeficiency disorders (such as severely
combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
antagonists are useful for treating or preventing autoimmune diseases and
inhibit the growth, progression and/or metastasis of cancers. They are
also used to activate, differentiate or proliferate cancerous cells or
tissues, and can be used to treat diseases associated with increased cell
survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
as sources for generating antibodies, as molecular weight markers. This
sequence represents the tumour necrosis factor receptor (TNFR) domain of
the human 4-1BB protein. The sequence was used in the characterisation of
the TR2 receptor protein of the invention
XX
SQ
Sequence 132 AA;
Query Match 75.8%; Score 47; DB 3; Length 132;
Best Local Similarity 72.7%; Pred. No. 1.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPGQELTKQG 11
Db 79 CRQGQELTKKG 89
RESULT 17
AAW31759
ID AAW31759 standard; protein; 219 AA.
XX
XX
AAW31759;
XX
XX
01-APR-1998 (first entry)
XX
XX
A novel human h4-1BBSV receptor.
XX
h4-1BBSV receptor; 4-1BB receptor splicing variant; endotoxin shock;
KW
tumour necrosis factor; TNF ligand; T-cell activation; inflammation;
KW
tumour prevention; viral infection; autoimmune disease;
cellular proliferation.
XX
XX
Homo sapiens.
XX
XX
Key Location/Qualifiers
FT Peptide 1..18 /note= "putative signal sequence"
FT Protein 19..219 /note= "mature protein"
FT Domain 19..150
FT Domain 151..177 /note= "soluble extracellular domain"
FT Domain 151..177 /note= "transmembrane domain"
XX
XX
WO9733898-A1.
XX
XX
18-SEP-1997.
XX
XX
15-MAR-1996; 96WO-US003587.
XX
XX
15-MAR-1996; 96WO-US003587.
XX
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
XX
Ni J, Yu G, Gentz RL;
XX

DR WPI: 1997-470806/43.
DR N-PSDB; AAT88969.
XX Human 4-1BB receptor splicing variant and related DNA - used to develop
PT products for treating e.g. tumours, viral infection, endotoxemic shock,
PT autoimmune disease or bone resorption.
XX
XX Claim 15; Fig 1; 73pp; English.
XX
CC The present sequence represents a novel human h4-1BBSV receptor. This is
CC a human 4-1BB receptor splicing variant. The 4-1BB ligand is a member of
CC the tumour necrosis factor (TNF) family of ligands. It is induced by T-
CC cell activation. The h4-1BBSV receptor nucleic acid and protein can be
CC used for diagnosis and therapy. In particular, agonists of h4-1BBSV
CC receptor can be used to treat and/or prevent tumours, restenosis,
CC cytotoxicity, bacterial and viral infection, deleterious effects of
CC ionising radiation, autoimmune disease, AIDS and graft-host rejection, to
CC regulate immune responses, wound healing and cellular proliferation.
CC Antagonists can be used to treat and/or prevent endotoxemic shock,
CC inflammation, cerebral malaria, activation of the HIV virus, graft
CC rejection, bone resorption and cachexia
XX
SQ Sequence 219 AA;
Query Match 75.8%; Score 47; DB 2; Length 219;
Best Local Similarity 72.7%; Pred. No. 3.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPQQLTKQG 11
Db 70 CKQQLTKKG 80
RESULT 18
AAW92523
ID AAW92523 standard; protein; 219 AA.
XX
AC AAW92523;
XX
XX 23-APR-1999 (first entry)
XX Human h4-1BBSV receptor protein.
XX
XX h4-1BBSV receptor; human; splice variant; antagonist; treatment;
XX disease prevention; endotoxemic shock; inflammation; cerebral malaria;
XX HIV virus activation; graft rejection; bone resorption; cachexia;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key 1..18
XX Peptide /label= signal_peptide
XX Protein 19..219
XX US5874240-A.
XX
XX 23-FEB-1999.
XX
XX 13-MAR-1997; 97US-00816605.
XX
XX 15-MAR-1996; 96US-0013474P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Dillon PJ, Yu G, Ni J, Gentz R;
XX WPI; 1999-179974/15.
XX N-PSDB; AAX02162.
XX New nucleic acid encoding human 4-1BB receptor splicing variant - useful
PT in treating h4-1BBSV mediated disease states such as endotoxemic shock,
PT inflammation, graft rejection and inactivation of HIV.

XX Claim 1a; Fig 1A-B; 28pp; English.
XX
CC This sequence represents a novel human h4-1BBSV receptor protein which is
CC used in a method for making a human 4-1BB receptor splice variant which
CC acts as an antagonist. The antagonist polypeptides may be used to
CC treat/prevent disease states mediated by h4-1BBSV receptors such as
CC endotoxemic shock, inflammation, cerebral malaria, activation of the HIV
CC virus, graft rejection, bone resorption and cachexia. The h4-1BBSV coding
CC sequences are useful in gene therapy
XX
SQ Sequence 219 AA;
Query Match 75.8%; Score 47; DB 2; Length 219;
Best Local Similarity 72.7%; Pred. No. 3.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPQQLTKQG 11
Db 70 CKQQLTKKG 80
RESULT 19
AAW92524
ID AAW92524 standard; protein; 219 AA.
XX
AC AAW92524;
XX
XX 23-APR-1999 (first entry)
XX Human h4-1BBSV receptor protein variant.
XX
XX h4-1BBSV receptor; human; splice variant; antagonist; treatment;
XX disease prevention; endotoxemic shock; inflammation; cerebral malaria;
XX HIV virus activation; graft rejection; bone resorption; cachexia;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 33..34
XX /note= "site of deletion of residues GTFCNDRNQICSPC
XX PNFSSAGGQRTCDICQCK corresponding to amino acid
XX residues 34-69 of the wild-type protein"
XX
XX US5874240-A.
XX
XX 23-FEB-1999.
XX
XX 13-MAR-1997; 97US-00816605.
XX
XX 15-MAR-1996; 96US-0013474P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Dillon PJ, Yu G, Ni J, Gentz R;
XX WPI; 1999-179974/15.
XX
XX New nucleic acid encoding human 4-1BB receptor splicing variant - useful
PT in treating h4-1BBSV mediated disease states such as endotoxemic shock,
PT inflammation, graft rejection and inactivation of HIV.
XX
XX Claim 29; Page; 28pp; English.
XX
CC This sequence represents a human h4-1BBSV receptor protein variant which
CC has antagonistic properties. This protein may be used to treat/prevent
CC disease states mediated by h4-1BBSV receptors such as endotoxemic shock,
CC inflammation, cerebral malaria, activation of the HIV virus, graft
CC rejection, bone resorption and cachexia. The h4-1BBSV coding sequences
CC are useful in gene therapy. This sequence does not appear in the
CC specification but has been created from the wild-type sequence

CC represented in Fig 2
 XX Sequence 219 AA;
 SQ

Query Match 75.8%; Score 47; DB 2; Length 219;
 Best Local Similarity 72.7%; Pred. No. 3.2;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 Db 70 CKQGQELTKKG 80

RESULT 20
 ID AAE08545 standard; protein; 219 AA.
 XX AAE08545;
 AC AAE08545;
 XX 15-NOV-2001 (first entry)
 DT Human h4-lbb splicing variant (h4-lbbsv) receptor.
 XX Human; h4-lbb receptor splicing variant; h4-lbbsv; gene therapy; tumour;
 KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotox shock;
 KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;
 KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;
 KW bone resorption; human immunodeficiency virus; HIV; graft rejection;
 KW inflammation; antibacterial; immunosuppressive; vulnery; vasotropic;
 KW antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.
 XX Homo sapiens.
 OS

Key Location/Qualifiers
 FT Peptide 1..18 /label= Signal_peptide
 FT Protein 19..219 /label= Mature_human_h4-lbbsv_receptor
 FT Domain 19..150 /label= Extracellular_domain
 FT Domain 151..177 /label= Transmembrane_domain
 XX US2001014465-A1.
 PN 16-AUG-2001.
 PD 19-DEC-2000; 2000US-00739394.
 PF 15-MAR-1996; 96US-0013474P.
 PR 13-MAR-1997; 97US-00816605.
 PR 22-FEB-1999; 99US-00253549.
 XX (NIJJ/) NI J.
 PA (YUGG/) YU G.
 PA (GENT/) GENTZ R. J.
 PA (DILL/) DILLON P. J.
 XX Ni J, Yu G, Gentz R, Dillion PJ;
 PI WPI; 2001-529104/58.
 DR N-PSDB; AAD15246.
 XX New human 4-lbb receptor splicing variant polypeptides and
 FT polynucleotides, useful for research, diagnosis, prevention and treatment
 PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
 PT syndrome and graft rejection.
 XX Claim 15; Fig 1; 28pp; English.
 PS The present invention relates to an isolated human 4-lbb receptor
 CC splicing variant (h4-lbbsv, where 4-lbb is a member of tumour necrosis
 CC factor (TNF) family of ligands) polypeptide. h4-lbbsv cdna is used in

Gene therapy. h4-lbbsv is useful for research, biological, clinical and
 therapeutic purposes. h4-lbbsv, its fragments, analogues or derivatives
 are useful as an immunogen to produce antibodies which are useful for
 isolating and identifying clones expressing the polypeptide or to purify
 the polypeptide. h4-lbbsv is useful for diagnosis and treatment of
 disorders of cells, tissues and organisms and its nucleic acid is useful
 for detecting complementary polynucleotides for e.g. as a diagnostic
 reagent and for chromosomal identification. h4-lbbsv receptor agonists
 are useful for preventing, treating tumours, restenosis, cytotoxicity,
 bacterial and viral infection, deleterious effects of ionising radiation,
 autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-
 host rejection, to regulate immune responses, wound healing and cellular
 proliferation and antagonists are useful for treating and/or preventing
 endotox shock, inflammation, cerebral malaria, activation of human
 immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
 cachexia. The present sequence is human h4-lbbsv receptor
 XX
 SQ Sequence 219 AA;
 Query Match 75.8%; Score 47; DB 4; Length 219;
 Best Local Similarity 72.7%; Pred. No. 3.2;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 Db 70 CKQGQELTKKG 80

RESULT 21
 ID ABB84639 standard; protein; 219 AA.
 XX ABB84639;
 AC ABB84639;
 XX 05-FEB-2003 (first entry)
 DT Human h4-lbbsv receptor.
 XX Human; h4-lbbsv receptor; anti-tumour; virucide; immunosuppressive;
 KW anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator;
 KW vasotropic; gene therapy; chromosome mapping; extracellular domain;
 KW endotox shock; cytotoxicity; cerebral malaria; autoimmune disease;
 KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;
 KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;
 KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;
 KW autoimmune disease.
 XX Homo sapiens.
 OS

Key Location/Qualifiers
 FT Peptide 1..18 /label= leader_sequence
 FT Protein 19..219 /label= h4-lbbsv_receptor
 FT Domain 19..150 /note= "region specifically claimed in claim 1b"
 FT Domain 151..177 /note= "region specifically claimed in claim 1a"
 FT Domain 151..177 /label= transmembrane_domain
 XX US2002127651-A1.
 PN 12-SEP-2002.
 PD 15-MAR-2002; 2002US-00097330.
 PF 15-MAR-1996; 96US-0013474P.
 PR 13-MAR-1997; 97US-00816605.
 PR 22-FEB-1999; 99US-00253549.
 PR 19-DEC-2000; 2000US-00739394.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA

XX PI Ni J, Yu G, Gentz RL, Dillon RJ;
XX DR WPI; 2003-066900/06.
XX DR N-PSDB; ABS57520.
XX PT Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,
XX PT providing resistance to bacteria, viruses and parasites, to induce
XX PT proliferation of endothelial cells, and to treat restenosis.
XX XX
XX PS Example 2; Fig 1A-B; 29pp; English.
XX CC This invention describes a novel human h4-1BBSV receptor or a sequence
XX CC that is at least 85% identical to the h4-1BBSV receptor. The product of
XX CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,
XX CC antibacterial, antiinflammatory, protozoacide, immunomodulator and
XX CC vasotropic activity and can be used for gene therapy and chromosome
XX CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to
XX CC a disease related to underexpression of h4-1BBSV or for identifying
XX CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV
XX CC receptor polypeptide is useful for treating and/or preventing endotoxic
XX CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human
XX CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or
XX CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired
XX CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,
XX CC viruses and parasites, to induce proliferation of endothelial cells and
XX CC certain haematopoietic cells, to treat restenosis and to prevent certain
XX CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.
XX CC This sequence represents the human 4-1BBSV receptor described in the
XX CC disclosure of the invention
XX CC
XX SQ Sequence 219 AA;
Query Match 75.8%; Score 47; DB 6; Length 219;
Best Local Similarity 72.7%; Pred. No. 3.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPQQLTKQG 11
|:|||||:
Db 70 CKQQLTKKG 80
RESULT 22
AAR64197
ID AAR64197 standard; protein; 255 AA.
AC AAR64197;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 08-AUG-1995 (first entry)
XX DE Human 4-1BB polypeptide.
XX KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
XX KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
XX OS Homo sapiens.
XX PN W09426290-A1.
XX PD 24-NOV-1994.
XX PF 06-MAY-1994; 94WO-US005036.
XX PR 07-MAY-1993; 93US-00060843.
XX PA (IMMV) IMMUNEX CORP.
XX PI Goodwin RG, Smith CA, Alderson MR;
XX DR WPI; 1995-022265/03.
XX DR N-PSDB; AAR75424.
XX XX

PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB
PT to transduce signal.
XX PS Claim 39; Page 47-48; 65pp; English.
XX CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAR75423)
XX CC are useful in a pharmaceutical composition for stimulating the immune
XX CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring
XX CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.
XX CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation
XX CC of primary T-cells during the derivation of clonal T-cell lines. It may
XX CC also be used to stimulate proliferation of activated T-cells, used in
XX CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 255 AA;
Query Match 75.8%; Score 47; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPQQLTKQG 11
|:|||||:
Db 106 CKQQLTKKG 116
RESULT 23
AAR70977
ID AAR70977 standard; protein; 255 AA.
AC AAR70977;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 16-OCT-1995 (first entry)
XX DE H4-1BB receptor protein.
XX KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
XX KW organ transplantation; cell membrane ligand.
XX OS Homo sapiens.
XX PN W09507984-A1.
XX PD 23-MAR-1995.
XX PF 15-SEP-1994; 94WO-US010457.
XX PR 16-SEP-1993; 93US-00122796.
XX PA (INDV) UNIV INDIANA FOUND.
XX PI Kwon BS;
XX DR WPI; 1995-131352/17.
XX DR N-PSDB; AAR86126.
XX PT Novel cDNA encoding human receptor protein H4-1BB - useful to produce the
XX PT protein which is used to treat auto-immune disease and facilitate organ
XX PT transplantation.
XX PS Claim 6; Fig 2; 36pp; English.
XX CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using
XX CC probes based on the mouse receptor protein 4-1BB gene. The PCR product
XX CC was used to screen a cDNA library of activated human T-cells. The
XX CC isolated cDNA (AAR86126), deposited as NRRL AAB21131, encoded the human
XX CC homolog H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct
XX CC PN field.)
XX SQ Sequence 255 AA;
Query Match 75.8%; Score 47; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.7;
XX XX

25-MAR-2003 (revised)

XXIX

666T-1999 (first en

ist entry)

DE Human receptor protein 4-1BB.
XX
XX Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation;
KW mouse 4-1BB cDNA; monoclonal antibody; immune response;
KW organ transplantation; autoimmune disease; diabetes; cancerous tumour;
KW rheumatoid arthritis; lupus; nerve growth factor receptor.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Protein 18..255
FT /note= "Purified human 4-1BB"
FT
XX
XX WO9936093-A1.
XX
XX 22-JUL-1999.
XX
XX 14-JAN-1999; 99WO-UB000823.
XX
XX 14-JAN-1998; 98US-00007097.
XX
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA (KWON/) KWON B S.
XX
XX Kwon BS;
XX
XX MPI: 1999-444325/37.
DR N-PSDB; AAZ08961.
XX
XX Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.
XX
XX Claim 4; Page 77-78; 86pp; English.
XX
XX The present sequence is a human receptor protein 4-1BB. 4-1BB is
CC structurally related to members of the nerve growth factor receptor. It
CC contains a putative zinc finger structure similar to that of yeast eIF-2b
CC protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of
CC H4-1BB. The H4-1BB protein, its ligands, and various monoclonal
CC antibodies have therapeutic uses. They may be used to enhance or suppress
CC T cell activation and proliferation; B cell proliferation; treating
CC cancerous tumors and AIDS. The use of H4-1BB to block H4-1BB ligand
CC binding has practical application in the suppression of immune system
CC during organ transplantation or against autoimmune diseases including
CC diabetes, rheumatoid arthritis, and lupus
XX
XX Sequence 255 AA;
SQ
Query Match 75.8%; Score 47; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPGQELTKQG 11
|:|||||:
DB 106 CKQGQELTKKG 116
RESULT 27
AAV33214
ID AAV33214 standard; protein; 255 AA.
XX
XX AAV33214;
XX
XX 18-NOV-1999 (first entry)
XX
XX Human CD137 protein.
XX
XX CD137; monocyte growth factor; proliferation; peripheral monocyte;
KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;
KW immunostimulatory; non-specific immune response; phagocytosis;
KW intracellular destruction; microorganism; immune complex; antibody;
KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
KW

KW bacterial; viral infection; immunosuppressant; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO9944629-A2.
XX
XX 10-SEP-1999.
XX
XX 05-MAR-1999; 99WO-EP001440.
XX
XX 05-MAR-1998; 98EP-00103859.
XX
XX (MERC) MERCKLE GMBH.
XX
XX Schwarz H, Langstein J;
PI
XX MPI: 1999-550983/46.
DR N-PSDB; AAZ09769.
XX
XX Use of monocyte growth factor CD137 for stimulating proliferation of
PT peripheral monocytes, particularly for treating immune deficiency, e.g.
PT following cancer therapy.
XX
XX Claim 12; Fig 1A; 57pp; German.
XX
XX This invention describes a novel use of the human monocyte growth factor
CC CD137, or its functional analogs, for (i) stimulating proliferation of
CC peripheral monocytes; and (ii) treating diseases that are associated with
CC disorders of a cellular system that includes monocytes (and/or their
CC derived cells, precursor or progenitors) or where the origin and/or
CC progression is treatable by stimulating proliferation of such cells. The
CC products of the invention have antitumor, antibacterial, antiviral,
CC antifungal and immunostimulatory activity. Stimulating proliferation of
CC monocytes promotes the non-specific immune response, i.e. it increases
CC phagocytosis and intracellular destruction of microorganisms, immune
CC complexes and damaged cells, and improves antibody (in)dependent
CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
CC diseases associated with a defective immune response where caused by
CC inadequate numbers of active monocytes/macrophages, especially damage to
CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation
CC therapy; disorders of wound healing (e.g. in dialysis or diabetic
CC patients, or those with chronic venous insufficiency); tumors; bacterial,
CC fungal or viral infections; (non-)congenital or (non-)inherited diseases
CC or injury to the immune system; injury induced by treatment with
CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune
CC disease, or transplant patients). Nucleic acid encoding (I) can be used
CC similarly, in gene therapy procedures. Proliferation of peripheral
CC monocytes is achieved independently of hematopoietic stem cells. This
CC sequence represents the human CD137 protein described in the method of
CC the invention
XX
XX Sequence 255 AA;
SQ
Query Match 75.8%; Score 47; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPGQELTKQG 11
|:|||||:
DB 106 CKQGQELTKKG 116
RESULT 28
AAE08546
ID AAE08546 standard; protein; 255 AA.
XX
XX AAE08546;
XX
XX 15-NOV-2001 (first entry)
XX
XX Human h4-1BB receptor.
XX
XX Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;
KW

KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;
 KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;
 KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;
 KW bone resorption; human immunodeficiency virus; HIV; graft rejection;
 KW inflammation; antibacterial; immunosuppressive; vulvar; vasotrophic;
 KW antiinflammatory; protozoicide; cachexia; immunomodulator; virucide.
 XX
 OS Homo sapiens.
 XX
 PN US2001014465-A1.
 XX
 PD 16-AUG-2001.
 XX
 XX 19-DEC-2000; 2000US-00739394.
 XX
 PF 15-MAR-1996; 96US-0013474P.
 PR 13-MAR-1997; 97US-0081660S.
 PR 22-FEB-1999; 99US-0025354S.
 XX
 XX (NIJ/J) NI J.
 PA (YUGG/) YU G.
 PA (GENT/) GENTZ R.
 PA (DILL/) DILLON P J.
 XX
 XX Ni J, Yu G, Gentz R, Dillon PJ;
 PI WPI; 2001-529104/58.
 XX
 DR New human 4-1BB receptor splicing variant polypeptides and
 XX polynucleotides, useful for research, diagnosis, prevention and treatment
 PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
 PT syndrome and graft rejection.
 XX
 PS Disclosure; Fig 2; 28pp; English.

XX The present invention relates to an isolated human 4-1BB receptor
 CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
 CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
 CC gene therapy. h4-1BBSV is useful for research, biological, clinical and
 CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives
 CC are useful as an immunogen to produce antibodies which are useful for
 CC isolating and identifying clones expressing the polypeptide or to purify
 CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of
 CC disorders of cells, tissues and organisms and its nucleic acid is useful
 CC for detecting complementary polynucleotides for e.g. as a diagnostic
 CC reagent and for chromosomal identification. h4-1BBSV receptor agonists
 CC are useful for preventing, treating tumours, restenosis, cytotoxicity,
 CC bacterial and viral infection, deleterious effects of ionising radiation,
 CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-
 CC host rejection, to regulate immune responses, wound healing and cellular
 CC proliferation and antagonists are useful for treating and/or preventing
 CC endotoxin shock, inflammation, cerebral malaria, activation of human
 CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
 CC cachexia. The present sequence is human h4-1BB receptor
 XX
 SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 4; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11
 | : | | | | | | | |
 Db 106 CKQGELTKKG 116

RESULT 29
 ID AAB50521
 XX AAB50521 standard; protein; 255 AA.
 AC AAB50521;
 XX
 XX 15-MAR-2001 (first entry)
 DT

XX
 DE
 XX
 XX
 KW Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.
 KW
 KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nontropic;
 KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
 KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
 KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
 KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
 KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
 KW apoptotic cell death related disease; autoimmune disorder;
 KW cardiovascular disorder; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200071150-A1.
 XX
 XX 30-NOV-2000.
 XX
 XX 18-MAY-2000; 2000WO-US013515.
 PF
 XX 20-MAY-1999; 99US-0135164P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Wei Y, Ruben SM, Gentz RL, Ni J;
 PI WPI; 2001-041051/05.
 XX
 DR Nucleic acid encoding a TRID polypeptide, also referred to as tumor
 XX necrosis factor receptor 5, useful in the diagnosis, treatment or
 PT prevention of cancer, autoimmune disorders and viral infection.
 PT
 XX Disclosure; Fig 2; 285pp; English.

XX The present invention describes the human TRID protein (tumour necrosis
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
 CC intracellular domain, also referred to as tumour necrosis factor receptor
 CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nontropic,
 CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotrophic
 CC activities, and can be used in gene therapy. The TRID polynucleotides are
 CC useful for detecting complementary polynucleotides. TRID proteins and
 CC polynucleotides are useful in the treatment of tumours, resistance to
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.
 CC They are also useful for inducing proliferation of T-cells, endothelial
 CC cells and certain haematopoietic cells, to regulate antiviral responses
 CC and to prevent certain autoimmune diseases after stimulation of TRID by
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
 CC polypeptides are useful for treating and/or preventing diseases
 CC associated with increased or decreased apoptotic cell death. The TRID
 CC polynucleotides, proteins, antibodies, agonists and antagonists are
 CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)
 CC autoimmune disorders; (c) diseases associated with increased apoptosis;
 CC (d) cardiovascular disorders; and (e) viral infection. The present
 CC sequence represents a tumour necrosis factor receptor used in comparison
 CC with TRID in the exemplification of the present invention
 XX
 SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 4; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11
 | : | | | | | | | |
 Db 106 CKQGELTKKG 116

RESULT 30
 ID ABB75955
 XX ABB75955 standard; protein; 255 AA.
 XX
 XX ABB75955;
 AC

XX 12-JUL-2002 (first entry)
DT ABR39863 standard; protein; 255 AA.
XX
DE Human cytokine receptor 4-1BB.
XX
KW Cytokine; receptor; 4-1BB; human.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
PH Key
FT Peptide 1..23
FT /label= signal_peptide
FT Protein 24..255
FT /label= Mature_protein
FT Domain 24..186
FT /note= "extracellular domain"
FT Modified-site 138..140
FT /note= "Asn is N-glycosylated"
FT Modified-site 149..151
FT /note= "Asn is N-glycosylated"
FT Region 186..213
FT /note= "transmembrane region"
FT Domain 214..255
FT /note= "cytoplasmic domain"
XX US6355779-B1.
XX
PN 12-MAR-2002.
XX
XX 10-SEP-1998; 98US-00150864.
XX
XX 07-MAY-1993; 93US-00060843.
XX 06-MAY-1994; 94US-00236918.
XX 05-AUG-1997; 97US-00910449.
XX
XX (IMMUNEX CORP.
XX
XX Goodwin RG, Smith CA, Alderson MR;
XX WPI; 2002-380940/41.
XX N-PSDB; ABL54048.
XX
XX New antibody specific for the cytokine 4-1BB-ligand, useful for
XX immunofluorescence purification of the ligand.
XX
XX Example 2; Col 43-44; 31pp; English.
XX
XX The present sequence is the protein sequence of the human cytokine
XX receptor, 4-1BB. The sequence was deduced from a cDNA clone (see
XX ABL54048) obtained from a human peripheral blood T-lymphocyte cDNA
XX library. It shows 60% identity to murine 4-1BB (see ABL75954). A portion
XX of the extracellular (ligand binding) domain of the human 4-1BB cytokine
XX receptor was utilised in a human 4-1BB/human IgG1 FC fusion protein,
XX which was used to identify the human 4-1BB ligand (4-1BB-L, see
XX ABL75953). The invention provides novel murine and human 4-1BB-L
XX polypeptides and human 4-1BB polypeptides, as well as DNA sequences
XX encoding them, recombinant expression vectors and host cells, and methods
XX for producing the novel polypeptides by cultivating the transformed host
XX cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from
XX their extracellular domains, have therapeutic value. Antibodies that are
XX immunoreactive with 4-1BB-L or human 4-1BB are claimed
XX
XX Sequence 255 AA;
XX
XX Query Match 75.8%; Score 47; DB 5; Length 255;
XX Best Local Similarity 72.7%; Pred. No. 3.7;
XX Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CRPQELTKQG 11
XX 106 CKQQLTKKG 116
XX
XX
XX

RESULT 31
ABR39863
ID ABR39863 standard; protein; 255 AA.
XX
XX ABR39863;
XX
XX 11-AUG-2003 (first entry)
XX
XX DE Human MOCEPTIN polypeptide.
XX
XX MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic;
XX antitipemic; antiarteriosclerotic; antidiabetic; cerebroprotective;
XX hypotensive; immunomodulator; antidepressant; human; receptor.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
PH Key
FT Peptide 1..17
FT /note= "putative signal peptide"
FT Protein 18..255
FT /note= "mature protein"
FT Domain 18..186
FT /note= "extracellular domain"
FT Domain 187..213
FT /note= "transmembrane domain"
FT Domain 214..255
FT /note= "intracellular domain"
XX
XX WO2003011325-A1.
XX
XX 13-FEB-2003.
XX
XX 25-JUL-2002; 2002WO-IB003499.
XX
XX 27-JUL-2001; 2001US-0308142P.
XX
XX (GEST) GENSET SA.
XX
XX Lucas J, Dialynas D, Briggs K;
XX WPI; 2003-268084/26.
XX N-PSDB; ACC47324.
XX
XX New agonist and antagonist of MOCEPTIN (a member of the Tumour Necrosis
XX Factor Receptor family) activity, useful for preventing or treating
XX obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing
XX body mass.
XX
XX Disclosure; Page 32-33; 37pp; English.
XX
XX The invention relates to an agonist or antagonist of MOCEPTIN (a member
XX of the Tumour Necrosis Factor Receptor family) activity. The antagonist
XX or agonist of MOCEPTIN activity, or the composition comprising the
XX agonist or antagonist, is useful for preventing or treating an obesity-
XX related disorder or disease in an individual. In particular, the agonist
XX of MOCEPTIN activity is useful for treating or preventing obesity-related
XX diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance, reducing
XX diabetes, stroke or hypertension. The agonist is also useful for reducing
XX body mass and maintaining weight loss. The antagonist of MOCEPTIN
XX activity is useful for increasing body mass, or for treating or
XX preventing disorders associated with excessive weight loss, e.g.
XX cachexia, cancer-related weight loss, AIDS-related weight loss, chronic
XX inflammatory disease-related weight loss, or anorexia. The present
XX sequence represents a human MOCEPTIN polypeptide
XX
XX Sequence 255 AA;
XX
XX Query Match 75.8%; Score 47; DB 6; Length 255;
XX Best Local Similarity 72.7%; Pred. No. 3.7;
XX Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CRPQELTKQG 11
XX
XX

Db 106 CKQQLTKKG 116

RESULT 32

AB884640

ID ABB84640 standard; protein; 255 AA.

XX AC ABB84640;

XX DT 05-FEB-2003 (first entry)

XX DE Human h4-1BB receptor.

XX KW Human; h4-1BSV receptor; anti-tumour; virucide; immunosuppressive; anti-HIV; antibacterial; anti-inflammatory; protozoacide; immunomodulator; vasotropic; gene therapy; chromosome mapping; extracellular domain; endotoxigenic shock; cytotoxicity; cerebral malaria; autoimmune disease; human immunodeficiency virus; HIV; graft-host rejection; bone resorption; cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome; AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis; autoimmune disease; h4-1BB.

XX OS Homo sapiens.

XX PN US2002127651-A1.

XX PD 12-SEP-2002.

XX PF 15-MAR-2002; 2002US-00097330.

XX PR 15-MAR-1996; 96US-0013474P.

XX PR 13-MAR-1997; 97US-00816605.

XX PR 22-FEB-1999; 99US-00253549.

XX PR 19-DEC-2000; 2000US-00739394.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Yu G, Gentz RL, Dillion PU;

XX WPI: 2003-066900/06.

XX PT Novel isolated h4-1BSV receptor polypeptide, useful for treating tumors, providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells, and to treat restenosis.

XX PS Disclosure; Fig 2; 29pp; English.

XX CC This invention describes a novel human h4-1BSV receptor or a sequence that is at least 85% identical to the h4-1BSV receptor. The product of the invention has anti-tumour, virucide, immunosuppressive, anti-HIV, antibacterial, anti-inflammatory, protozoacide, immunomodulator and vasotropic activity and can be used for gene therapy and chromosome mapping. h4-1BSV is useful for diagnosing a disease or susceptibility to a disease related to underexpression of h4-1BSV or for identifying agonists and antagonists. The soluble extracellular domain of h4-1BSV receptor polypeptide is useful for treating and/or preventing endotoxic shock, cytotoxicity, inflammation, cerebral malaria, activation of human immunodeficiency virus (HIV), graft-host rejection, bone resorption or cachexia, tumours, autoimmune disease, ionizing radiation, acquired immunodeficiency syndrome (AIDS), for providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells, and certain haematopoietic cells, to treat restenosis and to prevent certain autoimmune diseases after stimulation of h4-1BSV receptor by an agonist. This sequence represents the human h4-1BB receptor described in the disclosure of the invention

XX SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 6; Length 255;

Best Local Similarity 72.7%; Pred. No. 3.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQQLTKQG 11

Db 106 CKQQLTKKG 116

RESULT 33

AAE39531

ID AAE39531 standard; protein; 255 AA.

XX AC AAE39531;

XX DT 18-DEC-2003 (first entry)

XX DE Human protein SEQ ID NO: 2.

XX KW Human; adhesive; packaging.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 107

XX FT /note= "Encoded by AGA"

XX PN US2003000851-A1.

XX PD 02-JAN-2003.

XX PF 08-JUN-2001; 2001US-00877336.

XX PR 08-JUN-2001; 2001US-00877336.

XX PA (WALS/) WALSH J C.

XX PA (HAWK/) HAWKINS K E.

XX PI Walsh JC, Hawkins KE;

XX WPI: 2003-266968/26.

XX DR N-PSDB; AAD59981.

XX PT Paper board container manufacture for soap boxes, involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction.

XX PS Disclosure; Page 12-13; 46pp; English.

XX CC The invention relates to a method and apparatus for applying adhesive to packaging in a variety of configurations. The method involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction. The invention is useful for e.g. soap boxes, cereal boxes, bottle carriers, can boxes. The present sequence is human protein.

XX CC Note: There is no specific information about the sequence in the specification

XX SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 7; Length 255;

Best Local Similarity 72.7%; Pred. No. 3.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQQLTKQG 11

Db 106 CKQQLTKKG 116

RESULT 34

ADC78803

ID ADC78803 standard; protein; 255 AA.

XX AC ADC78803;

XX DT 01-JAN-2004 (first entry)

DE Human PRO protein #16.
 XX human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2003034984-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 15-OCT-2002; 2002WO-US033070.
 XX
 PR 19-OCT-2001; 2001US-0340083P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Gurney AL;
 XX WPI; 2003-481990/45.
 DR N-PSDB; ADC78802.
 XX
 PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 PT medicament for diagnosing or treating cancer or inflammatory bowel
 PT disorder e.g., ulcerative colitis or Crohn's disease.
 XX
 XX Claim 12; SEQ ID NO 32; 327pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for
 CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.
 XX
 SQ Sequence 255 AA;
 Query Match 75.8%; Score 47; DB 7; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRPQGLTKQG 11
 DB 106 CKQGOELTKKG 116
 RESULT 35
 ADD25599
 ID ADD25599 standard; protein; 255 AA.
 AC ADD25599;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Binding domain-immunoglobulin fusion protein-associated protein #77.
 XX
 KW Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN US2003118592-A1.
 XX
 PD 26-JUN-2003.
 XX
 PF 25-JUL-2002; 2002US-00207655.
 XX
 PR 17-JAN-2001; 2001US-0367358P.

PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX
 PA (GENE-) GENE-CRAFT INC.
 XX
 PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 XX WPI; 2003-801317/75.
 DR
 XX New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX
 XX Disclosure; SEQ ID NO 160; 157pp; English.
 XX
 CC The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID
 CC number therefore none of the sequences can be explicitly identified.
 XX
 SQ Sequence 255 AA;
 Query Match 75.8%; Score 47; DB 7; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRPQGLTKQG 11
 DB 106 CKQGOELTKKG 116
 RESULT 36
 ADE87541
 ID ADE87541 standard; protein; 255 AA.
 XX
 AC ADE87541;
 XX

DT 29-JAN-2004 (first entry)
 XX Unknown human receptor H4-1BB.
 XX
 KW immunosuppressive; H4-1BB ligand binding blocker; human;
 KW receptor protein; H4-1BB; B-cell proliferation stimulator;
 KW T-cell proliferation enhancer; immune system suppressor; transplantation;
 KW autoimmune disease.
 XX
 OS Homo sapiens.
 XX
 XX US2003082157-A1.
 XX
 XX PD 01-MAY-2003.
 XX
 XX PF 12-JUN-2002; 2002US-00170997.
 XX
 XX PR 07-NOV-1988; 88US-00267577.
 XX PR 30-JUL-1992; 92US-00922996.
 XX PR 01-FEB-1993; 93US-00012269.
 XX PR 05-JUN-1995; 95US-00460976.
 XX PR 22-OCT-1997; 97US-00955573.
 XX
 XX PA (KWON/) KWON B S.
 XX
 XX PI Kwon BS;
 XX
 XX DR WPI: 2003-576599/54.
 XX DR N-PSDB; ADE87540.
 XX
 XX PT New cDNA, or its encoded receptor protein H4-1BB, useful as probes to
 PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking
 PT H4-1BB ligand binding to facilitate organ transplantation or treat
 PT autoimmune diseases.
 XX
 XX PS Disclosure; SEQ ID NO 2; 19pp; English.
 XX
 CC The invention describes a cDNA, which encodes for human receptor protein
 CC H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe
 CC to isolate DNA sequences encoding for proteins similar to the receptor
 CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or
 CC derivatives, is useful as a probe for identifying ligands to the receptor
 CC protein H4-1BB, or for stimulating the proliferation of B-cells
 CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are
 CC useful for enhancing T-cell proliferation of activation. The cDNA or
 CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand
 CC binding, which is particularly useful for suppressing the immune system
 CC during transplantation, or for treating autoimmune diseases. This is the
 CC amino acid sequence of unknown human receptor H4-1BB.
 XX
 SQ Sequence 255 AA;
 Query Match 75.8%; Score 47; DB 7; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3, 7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRPQELTKQG 11
 Db 106 CKQGEELTKG 116
 RESULT 37
 AAEE29933
 ID AAEE29933 standard; protein; 265 AA.
 XX
 XX AC AAEE29933;
 XX
 XX DT 24-FEB-2003 (first entry)
 XX
 XX DE Human LP283 splice variant protein, LP346.
 XX
 XX KW Human; LP protein; cell proliferative disorder; actinic keratinosis;
 KW arteriosclerosis; psoriasis; leukaemia; lymphoma; autoimmune disorder;

KW melanoma; cancer; inflammatory disorder; Addison's disease; allergy;
 KW acquired immune deficiency syndrome; AIDS; ankylosing spondylitis;
 KW amyloidosis; anaemia; asthma; Crohn's disease; Goodpasture's syndrome;
 KW gout; Grave's disease; Hashimoto's thyroiditis; cardiovascular disorder;
 KW congestive heart failure; ischaemic heart disease; myocardial infarction;
 KW angina pectoris; arteriosclerosis; hypertension; neurological disorder;
 KW stroke; Parkinson's disease; Alzheimer's disease; developmental disorder;
 KW Down's syndrome; cerebral palsy; gene therapy; nephrotropic; nontropic.
 XX
 OS Homo sapiens.
 XX
 XX WO200274906-A2.
 XX
 XX PD 26-SEP-2002.
 XX
 XX PF 01-MAR-2002; 2002WO-US005093.
 XX
 XX PR 16-MAR-2001; 2001US-0276596P.
 XX PR 13-APR-2001; 2001US-0283654P.
 XX PR 20-APR-2001; 2001US-0285238P.
 XX PR 03-MAY-2001; 2001US-0288548P.
 XX PR 11-MAY-2001; 2001US-0290351P.
 XX
 XX PA (ELIL) LILLY & CO ELI.
 XX
 XX PI Amegadzie BY, Basinski MB, Chen D, Huang C, Keleher GP;
 XX Perkins DR, Rostock PRJ, Rowlinson SW, Sankhavaram PR, Seno ET;
 XX Su EW, Zhi Y;
 XX
 XX DR WPI: 2003-018798/01.
 XX
 XX PT New mammalian LP polynucleotides and proteins, useful in gene therapy,
 PT e.g. for treating or preventing cancers, autoimmune (e.g. AIDS),
 PT cardiovascular (e.g. myocardial infarction) or neurological (e.g. stroke)
 PT disorders.
 XX
 XX PS Claim 18; Page 286-287; 290pp; English.
 XX
 CC The present invention relates to LP (LP318a, LP318b, LP288, LP289, LP343,
 CC LP319a, LP319b, LP321, LP317, LP283, LP344, LP345 or LP346) proteins and
 CC polynucleotides encoding such proteins. Sequences of the invention are
 CC used to diagnose, treat or prevent cell proliferative disorders (e.g.
 CC actinic keratinosis, arteriosclerosis, psoriasis, leukaemia, lymphoma,
 CC melanoma, brain cancer or breast cancer), autoimmune or inflammatory
 CC disorders (e.g. AIDS (acquired immune deficiency syndrome), Addison's
 CC disease, allergies, ankylosing spondylitis, amyloidosis, anaemia, asthma,
 CC Crohn's disease, Goodpasture's syndrome, gout, Hashimoto's thyroiditis or
 CC Grave's disease), cardiovascular disorders (e.g. congestive heart
 CC failure, ischaemic heart disease, angina pectoris, myocardial infarction,
 CC atherosclerosis or hypertension), neurological disorders (e.g. stroke,
 CC Parkinson's disease or Alzheimer's disease) or developmental disorders
 CC (e.g. Down's syndrome or cerebral palsy). They are also used in gene
 CC therapy. The present sequence is human LP283 splice variant protein,
 CC LP346
 XX
 SQ Sequence 265 AA;
 Query Match 69.4%; Score 43; DB 6; Length 265;
 Best Local Similarity 88.9%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRPQELTK 9
 Db 184 CRPQELTK 192
 RESULT 38
 AAU02951
 ID AAU02951 standard; protein; 389 AA.
 XX
 XX AC AAU02951;
 XX
 XX DT 12-SEP-2001 (first entry)

XX DE Angiotensin converting enzyme (ACEV) splice variant protein #51.
XX KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
XX KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
XX KW platelet-derived endothelial cell growth factor; cardiovascular disease;
XX KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
XX KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
XX KW myocardial infarction; coronary arterial thrombosis; renal disease;
XX KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
XX KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
XX KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
XX KW vascular disorder; asbestosis.
XX OS Homo sapiens.
XX PN WO200136632-A2.
XX PD 25-MAY-2001.
XX PF 17-NOV-2000; 2000WO-IL000766.
XX PR 17-NOV-1999; 99IL-00132978.
XX PR 10-DEC-1999; 99IL-00133455.
XX PA (COMP-) COMPUGEN LTD.
XX PI Levine Z, David A, Azar I, Khostavi R, Bernstein J;
XX WPI; 2001-336004/35.
XX DR N-PSDB; AAS06051.
XX PT Novel alternative splicing variants e.g. variant of angiotensin
XX PT converting enzyme (ACEV), useful in identifying candidate compounds
XX PT capable of binding to the variant and to detect anti-variant antibodies.
XX PS Claim 4; Fig 51; 519pp; English.
XX CC The sequence represents an angiotensin converting enzyme splice variant
XX CC (ACEV) polypeptide. The polypeptides of the invention include variants of
XX CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
XX CC polypeptide receptor 2. The polypeptides and their associated nucleic
XX CC acids are useful for identification of variant sequences and detection of
XX CC candidate compounds capable of binding the molecules. The sequences of
XX CC the invention can be used in the treatment and diagnosis of various
XX CC disorders including cardiovascular diseases such as arteriosclerosis,
XX CC myocardial infarction and coronary arterial thrombosis, renal diseases
XX CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX CC immune disorders such as immune complex nephritis, multiple sclerosis,
XX CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such
XX CC as asbestosis and vascular pathologies involving an endothelial
XX CC abnormality such as deep vein thrombosis
XX CC Sequence 389 AA;
XX CC Query Match 69.4%; Score 43; DB 4; Length 389;
XX CC Best Local Similarity 72.7%; Pred. No. 30;
XX CC Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 CRPQELKQK 11
XX DB 367 CRPAQLQLQG 377
XX RESULT 39
XX AAG68259
XX ID AAG68259 standard; protein; 845 AA.
XX AC AAG68259;
XX XX
XX DT 14-FEB-2002 (first entry)

XX DE Human POLY6 protein sequence SEQ ID NO:12.
XX KW Human; POLYX; gamma aminobutyric acid receptor; GABA receptor;
KW epidermal growth factor; SGF; complement receptor; HSPC; syntaxin;
KW haematopoietic stem and progenitor cell; sulphotransferase; prohibitin;
KW antidepressant; cerebroprotective; antiparkinsonian; nootropic; relaxant;
KW anticonvulsant; neuroprotective; antiparkinsonian; nootropic; relaxant;
KW tranquilizer; antiarrhythmic; psychiatric; medical; depression; stroke;
KW Parkinson's disease; Huntington's disease; Tourette's syndrome; anxiety;
KW amyotrophic lateral sclerosis; head trauma; Alzheimer's disease;
KW alcoholism; vigilance; muscle tension; epileptogenic; memory function;
KW cardiomyopathy; arrhythmogenic right ventricular dysplasia.
XX OS Homo sapiens.
XX PN WO200179294-A2.
XX PD 25-OCT-2001.
XX PF 19-APR-2001; 2001WO-US012854.
XX PR 19-APR-2000; 2000US-0198293P.
XX PR 20-APR-2000; 2000US-0198645P.
XX PR 25-APR-2000; 2000US-0199476P.
XX PR 26-APR-2000; 2000US-0199880P.
XX PR 26-APR-2000; 2000US-0200024P.
XX PR 26-APR-2000; 2000US-0200025P.
XX PR 09-JUN-2000; 2000US-0210809P.
XX PR 17-JUL-2000; 2000US-0218591P.
XX PR 11-AUG-2000; 2000US-0224610P.
XX PR 09-FEB-2001; 2001US-0267673P.
XX PR 27-FEB-2001; 2001US-0271814P.
XX PA (CURA-) CURAGEN CORP.
XX PI Taupier RJ, Vernet CAM, Fernandes E, Shinkets RA, Majumder K;
XX PI Padigaru M, Colman SD, Zerhusen BD, Spytek KA, Burgess CS, Liu X;
XX WPI; 2002-017601/02.
XX DR N-PSDB; ABA03875.
XX PT New isolated polypeptides for treating a broad range of pathological
XX PT states, e.g., depression, stroke, Parkinson's disease, Huntington's
XX PT disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma,
XX PT and Alzheimer's.
XX PS Claim 1; Page 33-34; 155pp; English.
XX CC The present invention describes polypeptides (I), designated POLYX
XX CC polypeptides (e.g. POLY1, POLY2, etc.), and the polynucleotide sequences
XX CC (II) encoding them. POLY1-4 are members of the gamma aminobutyric acid
XX CC (GABA) receptor family; POLY5-8 are members of the epidermal growth
XX CC factor (EGF) family; POLY9-11 are members of the complement receptor
XX CC family; POLY12 is a member of the haematopoietic stem and progenitor cell
XX CC family; POLY13 is a member of the sulphotransferase family; POLY14
XX CC -16 are members of the syntaxin family; and POLY17 is a member of the
XX CC prohibitin family. (I) and (II) can have antidepressant,
XX CC cerebroprotective, antiparkinsonian, nootropic, relaxant, anticonvulsant,
XX CC neuroleptic, neuroprotective, antialcoholic, cardiant, tranquilliser and
XX CC antiarrhythmic activities. (I) and (II) can be used for treating or
XX CC preventing a POLYX-associated disorder in humans as a therapeutic in the
XX CC manufacture of a medicament for treating a syndrome associated with a
XX CC human disease selected from a POLYX-associated disorder, for treating a
XX CC pathological state in a mammal, especially patients suffering from, e.g.,
XX CC psychiatric and medical conditions, depression, stroke, Parkinson's
XX CC disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral
XX CC sclerosis, head trauma, Alzheimer's disease, alcoholism, vigilance,
XX CC anxiety, muscle tension, epileptogenic activity and memory functions,
XX CC cardiomyopathy and arrhythmogenic right ventricular dysplasia. The
XX CC present sequence represents POLY6
XX CC Sequence 845 AA;

Query Match 69.4%; Score 43; DB 5; Length 845;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
 |||||
 Db 55 CRPGFELTK 63

RESULT 40
 ABU12092
 ID ABU12092 standard; protein; 845 AA.
 XX
 AC ABU12092;
 XX
 DT 17-FEB-2003 (first entry)
 XX
 DE Novel human epidermal growth factor-like protein #2.
 XX
 KW Gamma-aminobutyric acid receptor-like protein; depression; stroke;
 KW GABA receptor-like protein; Parkinson's disease; Huntington's disease;
 KW Tourette's syndrome; amyotrophic lateral sclerosis; head trauma;
 KW Alzheimer's disease; alcoholism; vigilance; anxiety; muscle tension;
 KW epileptogenic activity; memory; cardiomyopathy; cancer; angiogenesis;
 KW arhythmogenic right ventricular dysplasia; renal disease; diabetes;
 KW Epidermal growth factor like protein; leukaemia; lupus; anaemia; ulcer;
 KW haematopoietic stem and progenitor cell like protein; cirrhosis;
 KW sulfoltransferase-like protein; cholangitis; hepatitis; hyperthyroidism;
 KW developmental disorder; Syntaxin-like protein; myxoid liposarcoma;
 KW asthma; Lambert-Eaton myasthenic syndrome; acute myeloid leukaemia;
 KW transgenic animal.
 XX
 OS Homo sapiens.
 XX
 XX US2002123612-A1.
 PN
 PD 05-SEP-2002.
 XX
 XX 03-JUL-2001; 2001US-00898570.
 PF
 PR 19-APR-2000; 2000US-0198293P.
 PR 20-APR-2000; 2000US-0198645P.
 PR 25-APR-2000; 2000US-0199476P.
 PR 26-APR-2000; 2000US-0199880P.
 PR 26-APR-2000; 2000US-0200024P.
 PR 26-APR-2000; 2000US-0200025P.
 PR 09-JUN-2000; 2000US-0210809P.
 PR 03-JUL-2000; 2000US-0215855P.
 PR 17-JUL-2000; 2000US-0218591P.
 PR 11-AUG-2000; 2000US-0224610P.
 PR 27-FEB-2001; 2001US-0271814P.
 XX
 XX (GERL/) GERLACH V L.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 XX
 PI Gerlach VL, Ellerman K, Macdougall JR, Smithson G;
 XX
 DR WPI; 2003-066815/06.
 DR N-PSDB; ABX56471.
 XX
 PT Novel polypeptides and nucleic acids which are members of epidermal
 PT growth factor, complement receptor families for diagnosing and treating
 PT psychiatric conditions, depression, stroke, Alzheimer's and Parkinson's
 PT disease.
 XX
 PS Claim 1; Page 20-21; 91pp; English.
 XX
 CC The invention describes an isolated POLYX (POLY1-17) polypeptide and its
 CC variant. POLYX polypeptides (especially POLY5, POLY6 and POLY7), the
 CC polynucleotides encoding them (I) and an anti-POLYX-antibody (III) are

CC useful for treating or preventing a pathology associated with POLYX
 CC polypeptide in humans and for treating a syndrome associated with human
 CC disease. POLYX polypeptide is also useful for identifying an agent that
 CC binds to POLYX and a cell expressing POLYX is useful for identifying a
 CC therapeutic agent for use in treatment of a pathology related to aberrant
 CC expression or physiological interactions of the polypeptide. (III) is
 CC useful for treating a pathological state in a mammal and for determining
 CC the presence or amount of POLYX in a sample. POLY1-4 (GABA receptor-like
 CC proteins) are useful for the treatment of psychiatric and medical
 CC conditions, depression, stroke, Parkinson's disease, Huntington's
 CC disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma,
 CC Alzheimer's disease, alcoholism, vigilance, anxiety, muscle tension,
 CC epileptogenic activity and memory functions, cardiomyopathy and
 CC arrhythmogenic right ventricular dysplasia. POLY5-8 (Epidermal growth
 CC factor like proteins) may be useful for treating cancer, aberrant
 CC angiogenesis, renal disease and diabetes. POLY12 (haematopoietic stem and
 CC progenitor cell like protein) may be useful for treatment of leukaemia,
 CC lupus and anaemia. POLY13 (sulfoltransferase-like protein) may be useful
 CC for treating cirrhosis, cholangitis, hepatitis, ulcers, hyperthyroidism
 CC and developmental disorders. POLY14-16 (Syntaxin-like proteins) may be
 CC useful in treatment of Lambert-Eaton myasthenic syndrome, asthma, myxoid
 CC liposarcoma and acute myeloid leukaemia, and POLY 18 may be useful in
 CC treatment of cancers. Cells comprising (I) are useful for producing non-
 CC human transgenic animals which are useful for studying the function
 CC and/or activity of POLYX protein and for identifying and/or evaluating
 CC modulators of POLYX protein activity. This is the amino acid sequence of
 CC a novel human protein
 XX
 SQ Sequence 845 AA;

Query Match 69.4%; Score 43; DB 6; Length 845;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
 |||||
 Db 55 CRPGFELTK 63

Search completed: May 5, 2004, 14:38:04
 Job time : 5.46233 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:35:32 ; Search time 1.58219 Seconds
(without alignments)
358.923 Million cell updates/sec

Title: US-10-067-122B-2_COPY_105_115

Perfect score: 62

Sequence: 1 CRPGQELTKQG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	4	US-08-012-269A-13
2	62	100.0	191	3	US-08-974-0222-52
3	62	100.0	191	3	US-08-795-445A-52
4	62	100.0	191	3	US-08-795-447A-52
5	62	100.0	191	3	US-08-974-186-52
6	62	100.0	191	3	US-08-795-446B-52
7	62	100.0	191	4	US-08-706-945D-139
8	62	100.0	191	4	US-08-577-788C-53
9	62	100.0	256	1	US-08-236-918A-6
10	62	100.0	256	4	US-09-150-864A-6
11	62	100.0	256	4	US-08-012-269A-2
12	62	100.0	256	4	US-08-623-545A-3
13	62	100.0	256	5	PCT-US96-03965-2
14	57	91.9	12	4	US-08-012-269A-7
15	47	75.8	132	4	US-08-523-323-55
16	47	75.8	219	2	US-08-816-605-9
17	47	75.8	255	1	US-08-236-918A-8
18	47	75.8	255	2	US-08-816-605-9
19	47	75.8	255	3	US-09-006-353A-11
20	47	75.8	255	4	US-09-007-097-2
21	47	75.8	255	4	US-09-150-864A-8
22	47	75.8	255	4	US-09-573-986-11
23	47	75.8	255	4	US-09-578-764A-2
24	47	75.8	255	4	US-09-623-545A-2
25	47	75.8	255	5	PCT-US96-03965-8
26	41	66.1	135	4	US-09-746-359A-70
27	41	66.1	196	4	US-09-746-359A-67

Sequence 59, Appl
Sequence 15, Appl
Sequence 58, Appl
Sequence 14, Appl
Sequence 57, Appl
Sequence 6, Appl
Sequence 3, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 28279, A
Sequence 36, Appl
Sequence 16, Appl
Sequence 481, App
Sequence 481, App

28 41 66.1 201 4 US-09-746-359A-59
29 41 66.1 203 4 US-09-746-359A-15
30 41 66.1 307 4 US-09-746-359A-58
31 41 66.1 311 4 US-09-746-359A-14
32 41 66.1 336 4 US-09-746-359A-57
33 40 64.5 297 4 US-09-548-130-6
34 40 64.5 299 4 US-09-548-130-3
35 40 64.5 299 4 US-10-119-466-12
36 39 62.9 228 3 US-08-911-423-2
37 39 62.9 228 4 US-09-512-363-7
38 39 62.9 228 4 US-09-176-200-7
39 37 59.7 151 3 US-09-286-529-4
40 37 59.7 210 3 US-09-286-529-3
41 37 59.7 504 4 US-08-253-91A-28279
42 37 59.7 1102 4 US-09-358-383C-36
43 37 59.7 1107 4 US-09-358-383C-16
44 36.5 58.9 59 4 US-09-461-325-481
45 36.5 58.9 59 4 US-10-012-542-481

ALIGNMENTS

RESULT 1
US-08-012-269A-13
; Sequence 13, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-012-269A-13

Query Match 100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred.No. 8.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
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Db 1 CRPGQELTKQG 11

RESULT 2
US-08-974-022-52
; Sequence 52, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,022
/ FILING DATE: 12-DEC-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/577,788
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winter, Robert B.
/ REFERENCE/DOCKET NUMBER: A-378
/ INFORMATION FOR SEQ ID NO: 52:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 191 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-974-022-52

Query Match 100.0%; Score 62; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
|||
Db 105 CRPGQELTKQG 115

RESULT 3

US-08-795-445A-52
; Sequence 52, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-445A-52

Query Match 100.0%; Score 62; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
|||
Db 105 CRPGQELTKQG 115

RESULT 4

US-08-795-447A-52
; Sequence 52, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-52

Query Match 100.0%; Score 62; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
|||
Db 105 CRPGQELTKQG 115

RESULT 5

US-08-974-186-52
; Sequence 52, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks

```
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-52

Query Match 100.0%; Score 62; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 105 CRPQOELTKQG 115

RESULT 6
US-08-795-446B-52
; Sequence 52, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-446B-52

Query Match 100.0%; Score 62; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 105 CRPQOELTKQG 115

RESULT 7
US-08-706-945D-139
; Sequence 139, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 139
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-706-945D-139

Query Match 100.0%; Score 62; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 105 CRPQOELTKQG 115

RESULT 8
US-08-577-788C-53
; Sequence 53, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 53
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Mus musculus
; US-08-577-788C-53

Query Match 100.0%; Score 62; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 105 CRPQOELTKQG 115
```

```
Db      105 CRPGQELTKQG 115

RESULT 9
US-08-236-918A-6
; Sequence 6, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-918A-6

Query Match      100.0%; Score 62; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      105 CRPGQELTKQG 115

RESULT 10
US-09-150-864A-6
; Sequence 6, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; TITLE OF INVENTION: That Binds Thereto
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18

Query Match      100.0%; Score 62; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      105 CRPGQELTKQG 115

RESULT 11
US-08-012-269A-2
; Sequence 2, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-012-269A-2

Query Match      100.0%; Score 62; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      105 CRPGQELTKQG 115

RESULT 12
US-09-623-545A-3
; Sequence 3, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; PROLIFERATION OF PERIPHERAL MONOCYTES
; FILE REFERENCE: 30424.1USWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-623-545A-3

Query Match      100.0%; Score 62; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CRPQELTKQG 11
|||||
Db 105 CRPQELTKQG 115

RESULT 13

PCT-US96-03965-2
; Sequence 2, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-Yuil
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03965
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA: US 08/012,269
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992

; PRIOR APPLICATION DATA: US 07/267,577
; APPLICATION NUMBER: 07-NOV-1988
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KW05

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US96-03965-2

Query Match 100.0%; Score 62; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11
|||||
Db 105 CRPQELTKQG 115

RESULT 14

US-08-012-269A-7
; Sequence 7, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.

; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An artificial peptide
US-08-012-269A-7

Query Match 91.9%; Score 57; DB 4; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.00069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11
|||||
Db 1 CRPQELTKSG 11

RESULT 15

US-09-523-323-55
; Sequence 55, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan

; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323

; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/168,380
; EARLIER FILING DATE: 1999-12-02
; EARLIER APPLICATION NUMBER: 60/148,326
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/142,657
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 60/137,457
; EARLIER FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: 60/124,041
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 09/252,656
; EARLIER FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: 60/075,409
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/027,287
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: 60/013,923
; EARLIER FILING DATE: 1996-03-22
; EARLIER APPLICATION NUMBER: 60/030,157
; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-523-323-55

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Query Match      75.8%; Score 47; DB 4; Length 132;
Best Local Similarity 72.7%; Pred. No. 0.49;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQGLTKQG 11
Db 79 CKQGQELTKKG 89

RESULT 16
US-08-816-605-2
; Sequence 2, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-605-2

Query Match      75.8%; Score 47; DB 2; Length 219;
Best Local Similarity 72.7%; Pred. No. 0.83;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQGLTKQG 11
Db 70 CKQGQELTKKG 80

RESULT 17
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

```

```

; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-918A-8

Query Match      75.8%; Score 47; DB 1; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQGLTKQG 11
Db 106 CKQGQELTKKG 116

RESULT 18
US-08-816-605-9
; Sequence 9, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512

```

```
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 255 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-816-603-9
;
Query Match          75.8%; Score 47; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 106 CKQGOELTKKG 116

RESULT 19
US-09-006-353A-11
; Sequence 11, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 255 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-09-006-353A-11
;
Query Match          75.8%; Score 47; DB 3; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 106 CKQGOELTKKG 116

RESULT 20
US-09-007-097-2
; Sequence 2, Application US/09007097A
; Patent No. 6303121
; GENERAL INFORMATION:
; APPLICANT: KWON, BYOUNG
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/007,097A
; CURRENT FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-007-097-2
;
Query Match          75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 106 CKQGOELTKKG 116

RESULT 21
US-09-150-864A-8
; Sequence 8, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens (clone: hu4-1BB)
; US-09-150-864A-8
;
Query Match          75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQOELTKQG 11
Db 106 CKQGOELTKKG 116

RESULT 22
US-09-573-986-11
; Sequence 11, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 255
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```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-11

Query Match      75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPQQLTKQG 11
Db      106 CKQQLTKKG 116

RESULT 23
US-09-578-764A-2
; Sequence 2, Application US/09578764A
; Patent No. 6569997
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/578,764A
; CURRENT FILING DATE: 2000-03-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-578-764A-2

```

```

Query Match      75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CRPQQLTKQG 11
Db      106 CKQQLTKKG 116

```

```

RESULT 24
US-09-623-545A-2
; Sequence 2, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; PROLIFERATION OF PERIPHERAL MONOCYTES
; FILE REFERENCE: 30424.1USWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-545A-2

```

```

Query Match      75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CRPQQLTKQG 11
Db      106 CKQQLTKKG 116

```

RESULT 25

```

PCT-US96-03965-8
; Sequence 8, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-Yuul
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03965
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KW05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-03965-8

```

```

Query Match      75.8%; Score 47; DB 5; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CRPQQLTKQG 11
Db      106 CKQQLTKKG 116

```

```

RESULT 26
US-09-746-359A-70
; Sequence 70, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.

```



```
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-70
```

```
Query Match 66.1%; Score 41; DB 4; Length 135;
Best Local Similarity 70.0%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 RPOGLTKQG 11
|||:|:|
Db 52 RPOGLTKQG 61
```

```
RESULT 27
US-09-746-359A-67
; Sequence 67, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprechter, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-67
```

```
Query Match 66.1%; Score 41; DB 4; Length 196;
Best Local Similarity 70.0%; Pred. No. 8.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 RPOGLTKQG 11
|||:|:|
Db 106 RPOGLTKQG 115
```

```
RESULT 28
US-09-746-359A-59
; Sequence 59, Application US/09746359A
; Patent No. 6610286
```

```
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprechter, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-59
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Query Match 66.1%; Score 41; DB 4; Length 201;
Best Local Similarity 70.0%; Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY 2 RPOGLTKQG 11
|||:|:|
Db 111 RPOGLTKQG 120
```

```
RESULT 29
US-09-746-359A-15
; Sequence 15, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprechter, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-15
```

```
Query Match 66.1%; Score 41; DB 4; Length 203;
Best Local Similarity 70.0%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 RPQQLTKQG 11
Db      111 RFGMEITKDG 120

RESULT 30
US-09-746-359A-58
; Sequence 58, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-58

Query Match      66.1%; Score 41; DB 4; Length 307;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 RPQQLTKQG 11
Db      111 RFGMEITKDG 120

RESULT 31
US-09-746-359A-14
; Sequence 14, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-14

Query Match      66.1%; Score 41; DB 4; Length 307;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 RPQQLTKQG 11
Db      111 RFGMEITKDG 120

RESULT 32
US-09-746-359A-57
; Sequence 57, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-57

Query Match      66.1%; Score 41; DB 4; Length 336;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 RPQQLTKQG 11
Db      140 RFGMEITKDG 149

RESULT 33
US-09-548-130-6
; Sequence 6, Application US/09548130
; Patent No. 6534081
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Van, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; FILE REFERENCE: P1739R1
; CURRENT APPLICATION NUMBER: US/09/548,130
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/128,849
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 297
```

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
| | | | | | | | | |
Db 21 CGPGQELSK 29

RESULT 36
US-08-911-423-2
; Sequence 2, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-2

Query Match 62.9%; Score 39; DB 3; Length 228;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTK 11
| | | | | | | | | |
Db 82 CGPGQEVESQG 92

RESULT 37
US-09-512-363-7
; Sequence 7, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TRIL, TRILSVL, and TRILSV2

TYPE: PRT
; ORGANISM: Human
US-09-548-130-6

Query Match 64.5%; Score 40; DB 4; Length 297;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
| | | | | | | | | |
Db 21 CGPGQELSK 29

RESULT 34
US-09-548-130-3
; Sequence 3, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P17391
; CURRENT APPLICATION NUMBER: US/09/548,130
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-548-130-3

Query Match 64.5%; Score 40; DB 4; Length 299;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
| | | | | | | | | |
Db 21 CGPGQELSK 29

RESULT 35
US-10-119-466-12
; Sequence 12, Application US/10119466
; Patent No. 6607899
; GENERAL INFORMATION:
; APPLICANT: Chui, Clarissa
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Milton, Sean
; APPLICANT: Yan, Minhong
; APPLICANT: Yi, Sothy
; TITLE OF INVENTION: CLONING METHOD
; FILE REFERENCE: P1797
; CURRENT APPLICATION NUMBER: US/10/119,466
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US/09/480,782
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 12
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Homo sapiens
; LOCATION: 1-299
; OTHER INFORMATION:
US-10-119-466-12

Query Match 64.5%; Score 40; DB 4; Length 299;
Best Local Similarity 77.8%; Pred. No. 20;

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; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; CURRENT FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; EARLIER APPLICATION NUMBER: 09/176,200
; EARLIER FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/121,648
; EARLIER FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: 60/134,172
; EARLIER FILING DATE: 1999-05-13
; EARLIER APPLICATION NUMBER: 60/144,076
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-512-363-7

Query Match      62.9%; Score 39; DB 4; Length 228;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CRPQELTKQG 11
Db      82 CQPGQRVESQG 92

RESULT 38
US-09-176-200-7
; Sequence 7, Application US/09176200
; Patent No.: 6509173
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/176,200
; CURRENT FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-176-200-7

Query Match      62.9%; Score 39; DB 4; Length 228;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CRPQELTKQG 11
Db      82 CQPGQRVESQG 92

RESULT 39
US-09-286-529-4
; Sequence 4, Application US/09286529
; Patent No.: 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 151
; TYPE: PRT
; ORGANISM: human
US-09-286-529-4

Query Match      59.7%; Score 37; DB 3; Length 151;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CRPQELTKQ 10
Db      53 CGPGMELSKE 62

RESULT 40
US-09-286-529-3
; Sequence 3, Application US/09286529
; Patent No.: 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 210
; TYPE: PRT
; ORGANISM: human
US-09-286-529-3

Query Match      59.7%; Score 37; DB 3; Length 210;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CRPQELTKQ 10
Db      52 CGPGMELSKE 61

Search completed: May 5, 2004, 14:42:16
Job time : 1.58219 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:40:42 ; Search time 4.06849 Seconds
(without alignments)
749.438 Million cell updates/sec

Title: US-10-067-122B-2_COPY_105_115

Perfect score: 62

Sequence: 1 CRPGQELTKQG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	14	US-10-067-122-13
2	62	100.0	191	11	US-09-405-032-136
3	62	100.0	256	13	US-10-027-199-10
4	62	100.0	256	14	US-10-067-122-2
5	57	91.9	12	14	US-10-067-122-7
6	47	75.8	132	15	US-10-375-680-55
7	47	75.8	219	9	US-09-739-394-2
8	47	75.8	219	13	US-10-097-330-2
9	47	75.8	255	9	US-09-739-394-9
10	47	75.8	255	9	US-09-826-212-11
11	47	75.8	255	9	US-09-935-727-13
12	47	75.8	255	10	US-09-877-336-2
13	47	75.8	255	13	US-10-097-330-9
14	47	75.8	255	13	US-10-027-199-2
15	47	75.8	255	14	US-10-170-997-2

16	47	75.8	255	14	US-10-186-643-11	Sequence 11, Appl
17	47	75.8	255	14	US-10-207-655-160	Sequence 160, Appl
18	47	75.8	255	15	US-10-418-242-13	Sequence 13, Appl
19	43	69.4	845	9	US-09-898-570-12	Sequence 12, Appl
20	43	69.4	845	10	US-09-839-446-12	Sequence 12, Appl
21	43	69.4	880	15	US-10-104-047-2834	Sequence 2834, Appl
22	43	69.4	897	14	US-10-239-663-35	Sequence 35, Appl
23	43	69.4	914	15	US-10-406-073-6	Sequence 6, Appl
24	43	69.4	974	9	US-09-898-570-14	Sequence 14, Appl
25	43	69.4	974	10	US-09-839-446-14	Sequence 14, Appl
26	43	69.4	993	14	US-10-239-663-36	Sequence 36, Appl
27	43	69.4	993	15	US-10-406-073-8	Sequence 8, Appl
28	43	69.4	993	15	US-10-406-073-15	Sequence 15, Appl
29	43	69.4	1006	11	US-09-930-512-18	Sequence 18, Appl
30	43	69.4	1009	9	US-09-898-570-16	Sequence 16, Appl
31	43	69.4	1009	10	US-09-839-446-16	Sequence 16, Appl
32	41	66.1	15	14	US-10-220-033-38	Sequence 38, Appl
33	41	66.1	135	9	US-09-746-359A-70	Sequence 70, Appl
34	41	66.1	135	15	US-10-424-658-70	Sequence 67, Appl
35	41	66.1	196	9	US-09-746-359A-67	Sequence 67, Appl
36	41	66.1	196	15	US-10-424-658-67	Sequence 59, Appl
37	41	66.1	201	9	US-09-746-359A-59	Sequence 16, Appl
38	41	66.1	201	9	US-09-912-672A-16	Sequence 35, Appl
39	41	66.1	201	10	US-09-925-055D-35	Sequence 59, Appl
40	41	66.1	201	15	US-10-424-658-59	Sequence 15, Appl
41	41	66.1	203	9	US-09-746-359A-15	Sequence 15, Appl
42	41	66.1	203	12	US-09-951-268-6	Sequence 5, Appl
43	41	66.1	203	15	US-10-424-658-15	Sequence 15, Appl
44	41	66.1	229	14	US-10-233-873A-2	Sequence 2, Appl
45	41	66.1	282	9	US-09-912-672A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-10-067-122-13
; Sequence 13, Application US/10067122
; Publication No. US20030100745A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/10/067,122
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 08/012,269
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-122-13

Query Match 100.0%; Score 62; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
Db 1 CRPGQELTKQG 11

RESULT 2
US-09-405-032-136
; Sequence 136, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:

APPLICANT: Amgen Inc.
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/405,032
FILING DATE: 24-Sep-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378-CIP2
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-405-032-136

Query Match 100.0%; Score 62; DB 11; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 105 CRPGQELTKQG 115

RESULT 3
US-10-027-199-10
; Sequence 10, Application US/10027199
; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
; METHOD
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-10-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1995-06-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1993-09-03
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-027-199-10

Query Match 100.0%; Score 62; DB 13; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 105 CRPGQELTKQG 115

RESULT 4
US-10-067-122-2
; Sequence 2, Application US/10067122
; Publication No. US20030100745A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/10/067,122
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 08/012,269
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-122-2

Query Match 100.0%; Score 62; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 105 CRPGQELTKQG 115

RESULT 5
US-10-067-122-7
; Sequence 7, Application US/10067122
; Publication No. US20030100745A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/10/067,122
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 08/012,269
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An artificial peptide
US-10-067-122-7

Query Match 91.9%; Score 57; DB 14; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 1 CRPGQELTKSG 11

RESULT 6
US-10-375-680-55
; Sequence 55, Application US/10375680

Publication No. US20040009147A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000E
CURRENT APPLICATION NUMBER: US/10/375,680
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,234
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-375-680-55

Query Match 75.8%; Score 47; DB 15; Length 132;
Best Local Similarity 72.7%; Pred. No. 1.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQQLTKQG 11
|:|||||:
Db 79 CKQQLTKKG 89

RESULT 7
US-09-739-394-2
Sequence 2, Application US/09739394
Patent No. US20010014465A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Yu, Guo-Liang
Gentz, Reiner

TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,394
FILING DATE: 19-Dec-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/253,549
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-739-394-2

Query Match 75.8%; Score 47; DB 9; Length 219;
Best Local Similarity 72.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQQLTKQG 11
|:|||||:
Db 70 CKQQLTKKG 80

RESULT 8
US-10-097-330-2
Sequence 2, Application US/10097330
Publication No. US20020127651A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
FILE REFERENCE: PF254D1C2
CURRENT APPLICATION NUMBER: US/10/097,330
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/739,394
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/253,549
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: US 08/816,605
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 60/013,474
PRIOR FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-330-2

Query Match 75.8%; Score 47; DB 13; Length 219;
Best Local Similarity 72.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQQLTKQG 11
|:|||||:
Db 70 CKQQLTKKG 80

RESULT 9
US-09-739-394-9
Sequence 9, Application US/09739394
Patent No. US20010014465A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Yu, Guo-Liang
Gentz, Reiner
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,394
FILING DATE: 19-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/253,549
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF254
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8512
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 255 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-09-739-394-9

Query Match 75.8%; Score 47; DB 9; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.4;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQGLTKQG 11
 |:|||||:
 Db 106 CKQQLTKKG 116

RESULT 10
 US-09-826-212-11
 ; Sequence 11, Application US/09826212
 ; Patent No. US20010021516A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wei, Ying-Pei
 ; APPLICANT: Gentz, Reiner
 ; APPLICANT: Ruben, Steven
 ; APPLICANT: Ni, Jian
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
 ; FILE REFERENCE: 1488.1280006
 ; CURRENT APPLICATION NUMBER: US/09/826,212
 ; CURRENT FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 11
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-212-11

Query Match 75.8%; Score 47; DB 9; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.4;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQGLTKQG 11
 |:|||||:
 Db 106 CKQQLTKKG 116

RESULT 11
 US-09-935-727-13
 ; Sequence 13, Application US/09935727
 ; Patent No. US20020150583A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
 ; FILE REFERENCE: PF454P2
 ; CURRENT APPLICATION NUMBER: US/09/935,727
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/303,224
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 60/252,131
 ; PRIOR FILING DATE: 2000-11-21
 ; PRIOR APPLICATION NUMBER: 60/227,598

; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: 09/518,931
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/168,235
 ; PRIOR FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: 60/146,371
 ; PRIOR FILING DATE: 1999-08-02
 ; PRIOR APPLICATION NUMBER: 60/131,964
 ; PRIOR FILING DATE: 1999-04-30
 ; PRIOR APPLICATION NUMBER: 60/131,270
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/124,092
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/121,774
 ; PRIOR FILING DATE: 1999-03-04
 ; PRIOR APPLICATION NUMBER: 09/006,352
 ; PRIOR FILING DATE: 1998-01-13
 ; PRIOR APPLICATION NUMBER: 60/035,496
 ; PRIOR FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-935-727-13

Query Match 75.8%; Score 47; DB 9; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.4;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQGLTKQG 11
 |:|||||:
 Db 106 CKQQLTKKG 116

RESULT 12
 US-09-877-336-2
 ; Sequence 2, Application US/09877336
 ; Publication No. US20030000851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kwon, Byoung
 ; TITLE OF INVENTION: METHODS OF USING HUMAN RECEPTOR ON
 ; FILE REFERENCE: 740.011US3
 ; CURRENT APPLICATION NUMBER: US/09/877,336
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: 09/007,097
 ; PRIOR FILING DATE: 1998-01-14
 ; PRIOR APPLICATION NUMBER: 08/409,851
 ; PRIOR FILING DATE: 1995-03-23
 ; PRIOR APPLICATION NUMBER: 08/122,796
 ; PRIOR FILING DATE: 1993-09-16
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-877-336-2

Query Match 75.8%; Score 47; DB 10; Length 255;
 Best Local Similarity 72.7%; Pred. No. 3.4;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPQGLTKQG 11
 |:|||||:
 Db 106 CKQQLTKKG 116

RESULT 13
 US-10-097-330-9
 ; Sequence 9, Application US/10097330


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; Publication No. US20020127651A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
; FILE REFERENCE: PF254D1C2
; CURRENT APPLICATION NUMBER: US/10/097,330
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/739,394
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/253,549
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: US 08/816,605
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 60/013,474
; PRIOR FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-330-9

Query Match 75.8%; Score 47; DB 13; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
Db 106 CKQGQELTKKG 116

RESULT 14
US-10-027-199-2
; Sequence 2, Application US/10027199
; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-199-2

Query Match 75.8%; Score 47; DB 13; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
Db 106 CKQGQELTKKG 116

RESULT 15
US-10-170-997-2
; Sequence 2, Application US/10170997
; Publication No. US20030082157A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: New Receptor and Related Products and
```

```

; Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/170,997
; FILING DATE: 12-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,573
; FILING DATE: 22-OCT-1997
; APPLICATION NUMBER: 08/460,976
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 13-SEP-1993
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; APPLICATION NUMBER: US 08/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KMO4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-170-997-2

Query Match 75.8%; Score 47; DB 14; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
Db 106 CKQGQELTKKG 116

RESULT 16
US-10-186-643-11
; Sequence 11, Application US/10186643
; Publication No. US20030118546A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/10/186,643
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-643-11

Query Match          75.8%; Score 47; DB 14; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 17
US-10-207-655-160
; Sequence 160, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 160
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-160

Query Match          75.8%; Score 47; DB 14; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

US-10-418-242-13
; Sequence 13, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P3
; CURRENT APPLICATION NUMBER: US/10/418,242
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,604
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,279
; PRIOR FILING DATE: 1999-04-27

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 13
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-13

Query Match          75.8%; Score 47; DB 15; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 19
US-09-898-570-12
; Sequence 12, Application US/09898570
; Patent No. US20020123612A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; FILE REFERENCE: 159666-776CIP
; CURRENT APPLICATION NUMBER: US/09/898,570
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/198,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/199,880
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/271,814
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/215,855
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 09/839,446
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 845
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
; OTHER INFORMATION: Z97832_B.0.707
US-09-898-570-12

Query Match          69.4%; Score 43; DB 9; Length 845;
Best Local Similarity 88.9%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTK 9
Db      55 CRPGFELTK 63
```

```
RESULT 20
US-09-839-446-12
; Sequence 12, Application US/09839446
; Publication No. US20030050232A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 15966-776
; CURRENT APPLICATION NUMBER: US/09/839,446
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/199,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/199,880
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/271,814
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 845
; TYPE: PRT
; ORGANISM: Unknown.Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
; OTHER INFORMATION: Z97832_B.0.707
US-09-839-446-12

Query Match      69.4%; Score 43; DB 10; Length 845;
Best Local Similarity 88.9%; Pred. No. 62;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTK 9
Db      55 CRPGFELTK 63

RESULT 21
US-10-104-047-2834
; Sequence 2834, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: H1-A0105
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2834
; LENGTH: 880
; TYPE: PRT

Query Match      69.4%; Score 43; DB 15; Length 880;
Best Local Similarity 88.9%; Pred. No. 65;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTK 9
Db      55 CRPGFELTK 63

RESULT 22
US-10-239-663-35
; Sequence 35, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, E.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-663-35

Query Match      69.4%; Score 43; DB 14; Length 897;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTK 9
Db      184 CRPGFELTK 192

RESULT 23
US-10-406-073-6
; Sequence 6, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: NG, Chi Kin Domingos
; APPLICANT: TOMLINSON, James E.
; APPLICANT: KOMTIVES, Laszlo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; TITLE OF INVENTION: PROPEINS IN VASCULAR ENDOTHELIUM
; FILE REFERENCE: MF102-048PIRNM
; CURRENT APPLICATION NUMBER: US/10/406,073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in version 3.1
US-10-406-073-6

Query Match      69.4%; Score 43; DB 10; Length 845;
Best Local Similarity 88.9%; Pred. No. 62;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTK 9
Db      55 CRPGFELTK 63
```

```
; FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-6
```

```
Query Match          69.4%; Score 43; DB 15; Length 914;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CRPGQELTK 9
Db 184 CRPGFELTK 192
```

```
RESULT 24
US-09-898-570-14
; Sequence 14, Application US/09898570
; Patent No. US20020123612A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; FILE REFERENCE: 15966-776CIP
; CURRENT APPLICATION NUMBER: US/09/898,570
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/198,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/199,880
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/271,814
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
```

```
US-09-898-570-14
```

```
; Sequence 14, Application US/09898570
; Patent No. US20020123612A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; FILE REFERENCE: 15966-776CIP
; CURRENT APPLICATION NUMBER: US/09/898,570
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/198,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/199,880
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/271,814
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/215,855
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 09/839,446
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
US-09-898-570-14
```

```
Query Match          69.4%; Score 43; DB 9; Length 974;
Best Local Similarity 88.9%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CRPGQELTK 9
Db 184 CRPGFELTK 192
```

```
RESULT 25
US-09-839-446-14
; Sequence 14, Application US/09839446
; Publication No. US20030050232A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; FILE REFERENCE: 15966-776
; CURRENT APPLICATION NUMBER: US/09/839,446
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/198,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/199,880
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/271,814
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
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```
US-09-839-446-14
```

```
; Sequence 14, Application US/09839446
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
```

```
Query Match          69.4%; Score 43; DB 10; Length 974;
Best Local Similarity 88.9%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CRPGQELTK 9
Db 184 CRPGFELTK 192
```

```
RESULT 26
US-10-233-663-36
; Sequence 36, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
```

; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-663-36

Query Match 69.4%; Score 43; DB 14; Length 993;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
||| |||
Db 184 CRPGFELTK 192

RESULT 27
US-10-406-073-8
; Sequence 8, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: NG, Chi Kin Domingos
; APPLICANT: TOMLINSON, James E.
; APPLICANT: KOMUVES, Laszlo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
; FILE REFERENCE: MPI02-048P1RM
; CURRENT APPLICATION NUMBER: US/10/406,073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-8

Query Match 69.4%; Score 43; DB 15; Length 993;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
||| |||
Db 184 CRPGFELTK 192

RESULT 28
US-10-406-073-15
; Sequence 15, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: NG, Chi Kin Domingos
; APPLICANT: TOMLINSON, James E.
; APPLICANT: KOMUVES, Laszlo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM

; FILE REFERENCE: MPI02-048P1RM
; CURRENT APPLICATION NUMBER: US/10/406,073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-15

Query Match 69.4%; Score 43; DB 15; Length 993;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
||| |||
Db 184 CRPGFELTK 192

RESULT 29
US-09-930-512-18
; Sequence 18, Application US/09930512
; Publication No. US20040010118A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly
; APPLICANT: Spaderna, Steven
; APPLICANT: Gangolli, Esha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Burgess, Catherine E
; APPLICANT: Majumder, Kumud
; APPLICANT: Sharmkets, Richard
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine
; APPLICANT: Szekeres, Edward S
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Liu, Xiaohong
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Ellerman, Karen
; APPLICANT: Smithson, Glenda
; APPLICANT: Peyman, John
; APPLICANT: Stone, David
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NO. US20040010118A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-091
; CURRENT APPLICATION NUMBER: US/09/930,512
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,692
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/225,837
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/225,693
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/226,236
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/226,353
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/227,085
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/227,395
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/227,492
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/227,600
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/275,952
; PRIOR FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-512-18

Query Match 69.4%; Score 43; DB 11; Length 1006;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9
||| |||
Db 219 CRPGFELTK 227

RESULT 30

US-09-898-570-16

; Sequence 16, Application US/09898570

; Patent No. US20020123612A1

; GENERAL INFORMATION:

; APPLICANT: GERLACH, VALERIE L.

; APPLICANT: ELLERMAN, KAREN

; APPLICANT: MACDOUGALL, JOHN R.

; APPLICANT: SMITHSON, GLENDA

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND

; TITLE OF INVENTION: METHODS OF USING THE SAME

; FILE REFERENCE: 15966-776CIP

; CURRENT APPLICATION NUMBER: US/09/898,570

; CURRENT FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 60/198,293

; PRIOR FILING DATE: 2000-04-19

; PRIOR APPLICATION NUMBER: 60/198,645

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: 60/210,809

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/199,476

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/200,025

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/224,610

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/200,024

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/199,880

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/218,591

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 60/271,814

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 60/215,855

; PRIOR FILING DATE: 2000-07-03

; PRIOR APPLICATION NUMBER: 09/839,446

; PRIOR FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 1009

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: POLYX

; OTHER INFORMATION: CG55096-04

US-09-898-570-16

Query Match 69.4%; Score 43; DB 9; Length 1009;

Best Local Similarity 88.9%; Pred. No. 75;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9
||| |||
Db 184 CRPGFELTK 192

RESULT 31

US-09-839-446-16

; Sequence 16, Application US/09839446

; Publication No. US20030050232A1

; GENERAL INFORMATION:

; APPLICANT: GERLACH, VALERIE L.

; APPLICANT: ELLERMAN, KAREN

; APPLICANT: MACDOUGALL, JOHN R.

; APPLICANT: SMITHSON, GLENDA

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND

; TITLE OF INVENTION: METHODS OF USING THE SAME

; FILE REFERENCE: 15966-776

; CURRENT APPLICATION NUMBER: US/09/839,446

; CURRENT FILING DATE: 2001-04-19

; PRIOR APPLICATION NUMBER: 60/198,293

; PRIOR FILING DATE: 2000-04-19

; PRIOR APPLICATION NUMBER: 60/198,645

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: 60/210,809

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/199,476

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/200,025

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/224,610

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/200,024

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/199,880

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/218,591

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 60/271,814

; PRIOR FILING DATE: 2001-02-27

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 1009

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: POLYX

; OTHER INFORMATION: CG55096-04

US-09-839-446-16

Query Match

Best Local Similarity 69.4%; Score 43; DB 10; Length 1009;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9
||| |||
Db 184 CRPGFELTK 192

RESULT 32

US-10-220-033-38

; Sequence 38, Application US/10220033

; Publication No. US20030186906A1

; GENERAL INFORMATION:

; APPLICANT: Schlingensiepen, Karl-Hermann

; APPLICANT: Schlingensiepen, Reimar

; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene

; TITLE OF INVENTION: and a molecule binding to an expression product of that

; TITLE OF INVENTION: gene

; FILE REFERENCE: P68119US0

; CURRENT APPLICATION NUMBER: US/10/220,033

; CURRENT FILING DATE: 2003-03-17

; PRIOR APPLICATION NUMBER: PCT/EP01/02694

; PRIOR FILING DATE: 2001-03-10

; PRIOR APPLICATION NUMBER: EP00105190.3

; PRIOR FILING DATE: 2000-03-11

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; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 38
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: obtained by screening randomly synthesized
; OTHER INFORMATION: peptides
US-10-220-033-38

```

```

Query Match          66.1%; Score 41; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

QY 2 RQOELTKQG 11
    |||||
DB 5 RQOELTKQG 14

```

```

RESULT 33
US-09-746-359A-70
; Sequence 70, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-70

```

```

Query Match          66.1%; Score 41; DB 9; Length 135;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 RQOELTKQG 11
    |||||
DB 52 RQOELTKQG 61

```

```

RESULT 34
US-10-424-658-70
; Sequence 70, Application US/10424658
; Publication No. US20040005320A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Blumberg, Hal
; APPLICANT: Chandrasekher, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation

```

```

; FILE REFERENCE: 99-108D1
; CURRENT APPLICATION NUMBER: US/10/424,658
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/746,359
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-424-658-70

```

```

Query Match          66.1%; Score 41; DB 15; Length 135;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 RQOELTKQG 11
    |||||
DB 52 RQOELTKQG 61

```

```

RESULT 35
US-09-746-359A-67
; Sequence 67, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-67

```

```

Query Match          66.1%; Score 41; DB 9; Length 196;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 RQOELTKQG 11
    |||||
DB 106 RQOELTKQG 115

```

```

RESULT 36
US-10-424-658-67
; Sequence 67, Application US/10424658
; Publication No. US20040005320A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny

```

; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Blumberg, Hal
; APPLICANT: Chandrasekhar, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108D1
; CURRENT APPLICATION NUMBER: US/10/424,658
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/ 746,359
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-424-658-67

Query Match 66.1%; Score 41; DB 15; Length 196;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQBELTKQG 11
|||:|:
Db 106 RRGMEITKDG 115

RESULT 37
US-09-746-359A-59
; Sequence 59, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-59

Query Match 66.1%; Score 41; DB 9; Length 201;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQBELTKQG 11
|||:|:
Db 111 RRGMEITKDG 120

RESULT 38

US-09-912-672A-16
; Sequence 16, Application US/09912672A
; Patent No. US20020164689A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
; TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 07334-184001
; CURRENT APPLICATION NUMBER: US/09/912,672A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/475,541
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-672A-16

Query Match 66.1%; Score 41; DB 9; Length 201;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQBELTKQG 11
|||:|:
Db 111 RRGMEITKDG 120

RESULT 39
US-09-925-055D-35
; Sequence 35, Application US/09925055D
; Publication No. US20030157096A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: SOLUBLE CYTOKINE RECEPTORS
; FILE REFERENCE: 00-56
; CURRENT APPLICATION NUMBER: US/09/925,055D
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/223,827
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 60/250,876
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-055D-35

Query Match 66.1%; Score 41; DB 10; Length 201;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQBELTKQG 11
|||:|:
Db 111 RRGMEITKDG 120

RESULT 40
US-10-424-658-59
; Sequence 59, Application US/10424658
; Publication No. US20040005320A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Blumberg, Hal
; APPLICANT: Chandrasekhar, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108D1


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; CURRENT APPLICATION NUMBER: US/10/424,658
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/ 746,359
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-424-658-59

Query Match      66.1%; Score 41; DB 15; Length 201;
Best Local Similarity 70.0%; Pred.No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2  RPQGLTKQG 11
Db      111  RPQGLTKQG 120
```

Search completed: May 5, 2004, 14:53:53
Job time : 4.06849 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:41 ; Search time 1.31849 Seconds
(without alignments)
802.512 Million cell updates/sec

Title: US-10-067-122B-2_COPY_105_115

Perfect score: 62

Sequence: 1 CRPGQELTKQG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	62	100.0	256	B32393	T-cell antigen 4-1
2	47	75.8	255	I38426	lymphocyte activat
3	39	62.9	684	T30652	probable RNA helic
4	38	61.3	413	1 VHVNIH	nucleoprotein - in
5	38	61.3	417	T34561	hypothetical prote
6	38	61.3	713	1 UMMS	period clock prote
7	38	61.3	1334	E86451	probable copia-typ
8	37	59.7	110	S52156	protamine - fruit
9	37	59.7	110	S52156	protamine - fruit
10	37	59.7	203	149054	ly-49G.2 antigen -
11	37	59.7	515	S54592	hypothetical prote
12	37	59.7	1102	T17367	potassium channel
13	37	59.7	1372	T25933	hypothetical prote
14	37	59.7	2871	A55624	fibillin-1 precur
15	36	58.1	202	A82148	30S ribosomal prot
16	36	58.1	404	1 VHVNHS	nucleoprotein - he
17	36	58.1	404	1 JQ1531	nucleoprotein - he
18	36	58.1	404	2 S34562	nucleosapsid prote
19	36	58.1	995	A56599	embryo kinase 5 -
20	36	58.1	1620	2 T27283	hypothetical prote
21	36	58.1	1894	2 J04980	plexin 1 precursor
22	36	58.1	2550	2 B33435	vesicular transpor
23	35	56.5	85	2 S21155	male germ-line spe
24	35	56.5	110	2 S21157	protamine - fruit
25	35	56.5	117	2 A50740	probable exported
26	35	56.5	129	2 S06075	unci protein - Vib
27	35	56.5	240	2 T49856	probable Alpl1 hom
28	35	56.5	285	1 C70873	probable enoyl-CoA
29	35	56.5	303	2 AH2016	hypothetical prote

ALIGNMENTS

RESULT 1

B32393
T-cell antigen 4-1BB precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: B32393; I48879
R:Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A:Title: cDNA sequence of two inducible T-cell genes.
A:Reference number: A32393; MUID:89184547; PMID:2784565
A:Accession: B32393
A:Molecule type: mRNA
A:Residues: 1-256 <KWO>
A:Cross-references: GB:J04492; NID:G201121; PIDN:AAA40167.1; PID:G201122
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
A:Reference number: I48879; MUID:94179805; PMID:8133039
A:Accession: I48879
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-256 <RES>
A:Cross-references: EMBL:U02567; NID:gl117783; PIDN:AAA93113.1; PID:g409178
C:Genetics:
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 100.0%; Score 62; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRPGQELTKQG 11
DB 105 CRPGQELTKQG 115

RESULT 2

I38426
lymphocyte activation-induced receptor ILA precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38426; J07072
R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R.
Eur. J. Immunol. 24, 2219-2227, 1994
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.
A:Reference number: I38426; MUID:94374434; PMID:8088337
A:Accession: I38426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A;Residues: 1-255 <RES>
 A;Cross-references: EMBL:U03397; NID:G571320; PIDN:AAA53133.1; PID:G571321
 R;Schwarz, H.; Tuckwell, J.; Lotz, M.
 Gene 134, 295-298, 1993
 A;Title: A receptor induced by lymphocyte activation (IIA): a new member of the human ne
 A;Reference number: JT0752; MUID:94085794; PMID:8262389
 A;Accession: JT0752
 A;Molecule type: mRNA
 A;Residues: 1-106, 'R', 108-255 <SCH>
 C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
 C;Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix
 C;Superfamily: CD27 antigen; NGF receptor repeat homology
 C;Keywords: Glycoprotein; phosphoprotein; receptor; transmembrane protein
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-255/Product: lymphocyte activation-induced receptor IIA #status predicted <NAT>
 F;187-213/Domain: transmembrane #status predicted <TM>
 F;138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict
 F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 75.8%; Score 47; DB 2; Length 255;
 Best Local Similarity 72.7%; Pred. No. 0.51;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 | : ||||| :
 Db 106 CKQGLTKQG 116

RESULT 3
 T30652
 Probable RNA helicase - Molluscum contagiosum virus 1
 N;Alternate names: MC050R
 C;Species: Molluscum contagiosum virus 1
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Nov-2000
 R;Accession: T30652
 R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
 Science 273, 813-816, 1996
 A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
 A;Reference number: Z20876; MUID:96325459; PMID:8670425
 A;Accession: T30652
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-684 <SEN>
 A;Cross-references: EMBL:U60315; NID:G1491943; PIDN:AA55178.1; PID:G1491993
 C;Superfamily: vaccinia virus 18 protein

Query Match 62.9%; Score 39; DB 2; Length 684;
 Best Local Similarity 63.6%; Pred. No. 37;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 | : ||||| :
 Db 117 CRPGLEUREAG 127

RESULT 4
 VHVNIH
 nucleoprotein - infectious hematopoietic necrosis virus
 N;Alternate names: nucleocapsid protein
 C;Species: infectious hematopoietic necrosis virus
 C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
 C;Accession: A31834
 R;Gilmore Jr., R.D.; Leong, J.C.
 Virology 167, 644-648, 1988
 A;Title: The nucleocapsid gene of infectious hematopoietic necrosis virus, a fish rhabdo
 A;Reference number: A31834; MUID:89073771; PMID:3201758
 A;Accession: A31834
 A;Molecule type: mRNA
 A;Residues: 1-413 <GIL>
 A;Cross-references: GB:J04321; NID:G331304; PIDN:AAA46240.1; PID:G331305
 C;Superfamily: infectious hematopoietic necrosis virus nucleoprotein
 C;Keywords: nucleocapsid; nucleoprotein

Query Match 61.3%; Score 38; DB 1; Length 413;
 Best Local Similarity 87.5%; Pred. No. 36;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQQLTK 9
 ||||| :
 Db 183 RPQQLTK 190

RESULT 5
 T34561
 hypothetical protein DKFP2434L1050.1 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T34561
 R;Pouska, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, October 1999
 A;Reference number: Z21540
 A;Accession: T34561
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-417 <POU>
 A;Cross-references: EMBL:AL122079
 A;Experimental source: adult testis; clone DKFP2434L1050
 C;Genetics:
 A;Note: DKFP2434L1050.1

Query Match 61.3%; Score 38; DB 2; Length 417;
 Best Local Similarity 66.7%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
 | : ||||| :
 Db 125 CRPGNNLTK 133

RESULT 6
 UMMS
 period clock protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000
 R;Accession: A24403
 R;Shin, H.S.; Bargiello, T.A.; Clark, B.T.; Jackson, F.R.; Young, M.W.
 Nature 317, 445-448, 1985
 A;Title: An unusual coding sequence from a Drosophila clock gene is conserved in vertebr
 A;Reference number: A24403; MUID:86014384; PMID:2413365
 A;Accession: A24403
 A;Molecule type: DNA
 A;Residues: 1-713 <SHI>
 A;Cross-references: GB:X02966; GB:M12039; NID:G55125; PIDN:CAA26710.1; PID:G1334150
 C;Comment: Mutations within the per locus of the fruit fly affect a variety of natural bi
 C;Comment: The serine residues of the S-G repeats found in certain proteoglycans are att
 C;Superfamily: period clock protein; EGF homology
 C;Keywords: circadian rhythm; tandem repeat
 F;41-77/Domain: EGF homology <EGF>

Query Match 61.3%; Score 38; DB 1; Length 713;
 Best Local Similarity 77.8%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
 ||||| :
 Db 64 CRPGFELAK 72

RESULT 7
 ES6451
 probable copia-type polyprotein, 28768-32772 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Superfamily: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: ES6451

R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 C:Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1998
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: E86451
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1334 <STO>
 A:Cross-references: GB:AB005172; NID:G10092575; PIDN:AAG12968.1; GSPDB:GNO0141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: retrovirus-related polyprotein

Query Match 61.3%; Score 38; DB 2; Length 1334;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PQQLTKQG 11
 |||||:
 Db 1096 PQQLTKAG 1104
 |||||:
 |||||:

RESULT 8
 S2156
 protamine - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1998
 A:Accession: S2156
 R:Russell, S.R.
 submitted to the EMBL Data Library, November 1994
 A:Description: Drosophila melanogaster mst35B genes encode very similar protamine like m
 A:Reference number: S2155
 A:Accession: S2156
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-110 <RUS>
 A:Cross-references: EMBL:Z46784; NID:g608697; PID:g608698
 C:Genetics:
 A:Gene: FlyBase:Mat35B
 A:Cross-references: FlyBase:FBgn0013301

Query Match 59.7%; Score 37; DB 2; Length 110;
 Best Local Similarity 54.5%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 1 CRPQQLTKQG 11
 |||||:
 Db 69 CAPSQKCSKQG 79
 |||||:
 |||||:

RESULT 9
 S2158
 protamine - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1998
 A:Accession: S2158
 R:Russell, S.R.
 submitted to the EMBL Data Library, November 1994
 A:Description: Drosophila melanogaster mst35B genes encode very similar protamine like m
 A:Reference number: S2155
 A:Accession: S2158
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <RUS>
 A:Cross-references: EMBL:Z46785; NID:g608701; PID:g608702
 C:Genetics:

A:Gene: FlyBase:Mat35B
 A:Cross-references: FlyBase:FBgn0013301

Query Match 59.7%; Score 37; DB 2; Length 110;
 Best Local Similarity 54.5%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 1 CRPQQLTKQG 11
 |||||:
 Db 69 CAPSQKCSKQG 79
 |||||:
 |||||:

RESULT 10
 I49054
 Ly-49G.2 antigen - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Mar-2000
 A:Accession: I49054
 R:Smith, H.R.; Karhofer, F.M.; Yokoyama, W.M.
 J. Immunol. 153, 1068-1079, 1994
 A:Title: Ly-49 multigene family expressed by IL-2-activated NK cells.
 A:Reference number: I49049; MUID:94300069; PMID:8027540
 A:Accession: I49054
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-203 <RES>
 A:Cross-references: EMBL:U10095; NID:g533497; PIDN:AAA50223.1; PID:g533498
 C:Superfamily: natural killer cell receptor P1; C-type lectin homology

Query Match 59.7%; Score 37; DB 2; Length 203;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPQQLTK 9
 |||||:
 Db 109 CRPGNDLJK 117
 |||||:
 |||||:

RESULT 11
 S54592
 hypothetical protein YMR285c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YMR021.11c
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
 A:Accession: S54592; A42461
 R:Pearson, D.; Bowman, S.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54582
 A:Accession: S54592
 A:Molecule type: DNA
 A:Residues: 1-515 <PEA>
 A:Cross-references: EMBL:Z49704; NID:g825540; PID:g825551; MIPS:YMR285c
 A:Experimental source: strain AB972
 R:Kang, W.; Matsushita, Y.; Grohmann, L.; Graack, H.R.; Kitakawa, M.; Isono, K.
 J. Bacteriol. 173, 4013-4020, 1991
 A:Title: Cloning and analysis of the nuclear gene for Yml33, a protein of the large subur
 A:Reference number: A42461; MUID:91286184; PMID:2061283
 A:Accession: A42461
 A:Molecule type: DNA
 A:Residues: 1-68, 'A', 70-86, 'W', 88, 'ARAA', 93, 'YOKT', 98-105, 'Q' <KAN>
 A:Cross-references: GB:D90217
 C:Genetics:
 A:Gene: SGD:NGL2
 A:Cross-references: SGD:S0004898
 A:Map position: 13R
 C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC9B6.11c

Query Match 59.7%; Score 37; DB 2; Length 515;
 Best Local Similarity 47.1%; Pred. No. 68;
 Matches 8; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 1 CR-----PQQLTKQG 11
 |||||:
 |||||:

Db 477 CRGFLRMPGNEMTKHG 493

RESULT 12

potassium channel protein elkl - rat
T17367
C/Species: Rattus norvegicus (Norway rat)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T17367
R/Shi, W.; Wang, H.S.; Pan, Z.; Wymore, R.; Cohen, I.S.; McKinnon, D.; Dixon, J.E.
J. Physiol. 511, 675-682, 1998
A/Title: Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in
A/Reference number: Z18731; MUID:98382545; PMID:9714851
C/Accession: T17367
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1102 <SHI>
A/Cross-references: EMBL:AF061957; NID:G3659689; PID:G3659690; PIDN:AAC61520.1
C/Genetics:
A/Gene: elkl
C/Function:
A/Description: may play a role in the sympathetic nervous system
C/Keywords: potassium channel

Query Match 59.7%; Score 37; DB 2; Length 1102;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
| | | | |
Db 572 CAPGEVLLRQG 582

RESULT 13

T25933
hypothetical protein W02C12.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T25933
R/Murray, J.; Wohldmann, P.
Submitted to the EMBL Data Library, December 1996
A/Description: The sequence of C. elegans cosmid W02C12.
A/Reference number: Z20112
A/Accession: T25933
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1372 <MUR>
A/Cross-references: EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN000022; CBSP:W02C12.1
A/Experimental source: strain Bristol N2; clone W02C12
C/Genetics:
A/Gene: CBSP:W02C12.1
A/Map position: 4
A/Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1

Query Match 59.7%; Score 37; DB 2; Length 1372;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 10
| | | | |
Db 1098 CRPGQFLVKE 1107

RESULT 14

A55624
fibrillin-1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 24-Nov-2003
C/Accession: A55624
R/Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez,
J. Biol. Chem. 270, 1798-1806, 1995
A/Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ge
A/Reference number: A55624; MUID:95130561; PMID:7829516

A/Accession: A55624
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-2871 <YIN>
A/Cross-references: GB:L29454; NID:G575509; PIDN:AAA56840.1; PID:G575510
C/Genetics:
A/Gene: Fbn-1
C/Superfamily: fibrillin; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 59.7%; Score 37; DB 2; Length 2871;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
| | | | |
Db 1835 CRPGVRLTGTG 1845

RESULT 15

AB2148
30S ribosomal protein S4 [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C/Accession: AB2148
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AB2148
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-202 <KUR>
A/Cross-references: GB:BA000019; PIDN:BA074436.1; PID:G17131830; GSPDB:GN00179
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: rps4
C/Superfamily: Escherichia coli ribosomal protein S4

Query Match 58.1%; Score 36; DB 2; Length 202;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQEL 7
| | | | |
Db 131 CRPGEEI 137

RESULT 16

VHVNH5
nucleoprotein - hemorrhagic septicemia virus
N/Alternate names: nucleocapsid protein
C/Species: hemorrhagic septicemia virus
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C/Accession: A36651
R/Bernard, J.; Lecocq-Xhonneux, F.; Rossius, M.; Thierry, M.E.; de Kinkelin, P.
J. Gen. Virol. 71, 1669-1674, 1990
A/Title: Cloning and sequencing the messenger RNA of the N gene of viral haemorrhagic se
A/Reference number: A36651; MUID:90362052; PMID:2202782
A/Accession: A36651
A/Molecule type: mRNA
A/Residues: 1-404 <BER>
A/Cross-references: GB:D00687; NID:G222771; PIDN:BAA00591.1; PID:G222772
C/Genetics:
A/Gene: N
C/Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C/Keywords: nucleocapsid; nucleoprotein

Query Match 58.1%; Score 36; DB 1; Length 404;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQQLTK 9
| | | | |
Db 184 RPQQLTK 191

RESULT 17
JQ1531
nucleoprotein - hemorrhagic septicaemia virus (strain Makah)
N/Alternate names: nucleocapsid protein
C/Species: hemorrhagic septicaemia virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C/Accession: JQ1531, S21836
R/Bernard, J.; Bremont, M.; Winton, J.
J. Gen. Virol. 73, 1011-1014, 1992
A/Title: Nucleocapsid gene sequence of a North American isolate of viral haemorrhagic se
A/Reference number: JQ1531; MUID:92341050; PMID:1634868
A/Accession: JQ1531
A/Molecule type: mRNA
A/Residues: 1-404 <BER>
A/Cross-references: EMBL:X59241; NID:g60410; PIDN:CAA41930.1; PID:g60411
C/Genetics:
A/Gene: N
C/Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C/Keywords: nucleocapsid, nucleoprotein

Query Match 58.1%; Score 36; DB 1; Length 404;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQQLTK 9
| | | | |
Db 184 RPQQLTK 191

RESULT 18
S34562
nucleocapsid protein - hemorrhagic septicaemia virus
C/Species: hemorrhagic septicaemia virus
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C/Accession: S34562
R/Schuetze, H.
submitted to the EMBL Data Library, June 1993
A/Reference number: S34562
A/Accession: S34562
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-404 <SCH>
A/Cross-references: EMBL:X73873; NID:g395126; PIDN:CAAS2077.1; PID:g395127
C/Genetics:
A/Gene: n
C/Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C/Keywords: nucleocapsid

Query Match 58.1%; Score 36; DB 2; Length 404;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQQLTK 9
| | | | |
Db 184 RPQQLTK 191

RESULT 19
A56599
embryo kinase 5 - chicken
N/Alternate names: receptor tyrosine kinase Ceks
N/Contains: protein-tyrosine kinase (EC 2.7.1.112)
C/Species: Gallus gallus (chicken)
C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 04-Feb-2000
C/Accession: A56599
R/Pasquale, E.B.
Cell Regul. 2, 523-534, 1991

A/Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor-
A/Reference number: A56599; MUID:92144672; PMID:1664238
A/Accession: A56599
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-995 <PAS>
A/Cross-references: GB:M62325; NID:g211448; PIDN:AAA48667.1; PID:g211449
A/Note: sequence extracted from NCBI backbone (NCBIN:81999, NCBI:82001)
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat hc
C/Keywords: Atp; phosphotransferase; transmembrane protein; tyrosine-specific protein kin
F:628-896/Domain: protein kinase homology <KIN>
F:636-644/Region: protein kinase Atp-binding motif
F:919-985/Domain: SAM homology <SAM>

Query Match 58.1%; Score 36; DB 2; Length 995;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPQQLTKQG 11
| | | | |
Db 264 CRPQVESVENG 274

RESULT 20
T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T27283
R/Ainscough, R.
submitted to the EMBL Data Library, September 1999
A/Reference number: Z20336
A/Accession: T27283
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1620 <WIL>
A/Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f
A/Experimental source: Clone Y64G10A
C/Genetics:
A/Gene: CESP:Y64G10A.f
A/Introns: 77/1, 116/1, 198/1, 282/1, 365/1, 425/1, 466/1, 548/1, 559/1, 601/1, 625/1, 71

Query Match 58.1%; Score 36; DB 2; Length 1620;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPQQLTKQG 11
| | | | |
Db 492 CRPQFELSDG 502

RESULT 21
JC4980
plexin 1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Nov-1999
C/Accession: JC4980
R/Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa,
Biochem. Biophys. Res. Commun. 226, 524-529, 1996
A/Title: Identification of a neuronal cell surface molecule, plexin, in mice.
A/Reference number: JC4980; MUID:96400291; PMID:8806667
A/Accession: JC4980
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1894 <KAM>
A/Cross-references: DDBJ:D86948; NID:g1665756; PIDN:BAA13189.1; PID:di013877; PID:g16657
A/Experimental source: brain
C/Comment: This protein is a membrane protein, and plays a role in neuronal cell contact
ence of calcium ions.
C/Keywords: duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:513-561,659-704,807-859/Region: cysteine-rich
F:1238-1264/Domain: transmembrane #status predicted <TM>

F:1266-1268/Region: hydrophilic

Query Match 58.1%; Score 36; DB 2; Length 1894;
 Best Local Similarity 77.8%; Pred. No. 3.3e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RFGQELTKQ 10
 |||||
 Db 317 RFGQALAKQ 325

RESULT 22

B53435
 vesicular transport-associated repeat protein Tb-292 - Trypanosoma brucei
 N:Alternate names: membrane-associated protein Tb-292
 C:Species: Trypanosoma brucei
 C>Date: 28-May-1995 #sequence_revision 07-Jul-1995 #text_change 07-May-1999
 C:Accession: B53435; S34395
 R:Lee, M.G.S.; Russell, D.G.; D'Alessandro, P.A.; Van der Ploeg, L.H.T.
 J. Biol. Chem. 269, 8408-8415, 1994
 A:Title: Identification of membrane-associated proteins in Trypanosoma brucei encoding a
 A:Reference number: A53435; MUID:94179225; PMID:8132566
 A:Accession: B53435
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-189,558-721,'P',723-738,'D',740-829,'L',831-1100,'Q',1102-1636,'L',1638-16
 418,'H',2420-2499,'L',2501-2550 <LE2>
 A:Cross-references: EMBL:X73956
 R:Lee, M.; Russell, D.; D'Alessandro, P.; van der Ploeg, L.
 Submitted to the EMBL Data Library, December 1992
 A:Description: Identification of membrane associated proteins in Trypanosoma brucei encod
 A:Reference number: S34394
 A:Accession: S34395
 A:Molecule type: mRNA
 A:Residues: 1-2550 <LEE>
 A:Cross-references: EMBL:X73956; NID:g393395; PID:g393396
 C:Keywords: tandem repeat
 F:774-557/Region: 8-residue repeats (A-R-L-R-A-E-E)

Query Match 58.1%; Score 36; DB 2; Length 2550;
 Best Local Similarity 63.6%; Pred. No. 4.3e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11
 |||||
 Db 1470 CRPHSENTDQ 1480

RESULT 23

S52155
 male germ-line specific protamine - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1998
 C:Accession: S52155
 R:Russell, S.R.
 submitted to the EMBL Data Library, November 1994
 A:Description: Drosophila melanogaster mst35B genes encode very similar protamine like m
 A:Reference number: S52155
 A:Accession: S52155
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-85 <RUS>
 A:Cross-references: EMBL:Z46790; NID:g608695; PID:g608696
 C:Genetics:
 A:Gene: FlyBase:Mst35Ba
 A:Cross-references: FlyBase:FBgn0013300

Query Match 56.5%; Score 35; DB 2; Length 85;
 Best Local Similarity 54.5%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11
 |||||

Db 44 CAPRQCKSQG 54

RESULT 24

S52157
 protamine - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1998
 C:Accession: S52157
 R:Russell, S.R.
 submitted to the EMBL Data Library, November 1994
 A:Description: Drosophila melanogaster mst35B genes encode very similar protamine like m
 A:Reference number: S52157
 A:Accession: S52157
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <RUS>
 A:Cross-references: EMBL:Z46783; NID:g608699; PID:g608700
 C:Genetics:
 A:Gene: FlyBase:Mst35Ba
 A:Cross-references: FlyBase:FBgn0013300

Query Match 56.5%; Score 35; DB 2; Length 110;
 Best Local Similarity 54.5%; Pred. No. 40;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11
 |||||
 Db 69 CAPRQCKSQG 79

RESULT 25

AE0740
 probable exported protein STY2079 [imported] - Salmonella enterica subsp. enterica serove
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AE0740
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moulder, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AE0740
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05624.1; PID:g16503121; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY2079
 C:Superfamily: Escherichia coli hypothetical protein b1839

Query Match 56.5%; Score 35; DB 2; Length 117;
 Best Local Similarity 85.7%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQEL 7
 |||||
 Db 47 CRPGQAL 53

RESULT 26

S06075
 unci protein - Vibrio alginolyticus
 C:Species: Vibrio alginolyticus
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Oct-1999
 C:Accession: S06075
 R:Krumholz, L.R.; Esser, U.; Simoni, R.D.
 Nucleic Acids Res. 17, 7993-7994, 1989
 A:Title: Nucleotide sequence of the unc operon of Vibrio alginolyticus.
 A:Reference number: S06075; MUID:90016889; PMID:2529481

A;Accession: S06075
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-129 <RRU>
A;Cross-references: EMBL:X16050; NID:g48331; PIDN:CAA34174.1; PID:g48332
C;Genetics:
A;Gene: unci
C;Superfamily: unci protein

Query Match 56.5%; Score 35; DB 2; Length 129;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQLTKQ 10
|||:|:|:
Db 7 RPQQLTKQ 15

RESULT 27
T49856
Probable Alpl1 homolog of tubulin-folding cofactor B [imported] - Neurospora crassa
N;Alternate names: protein B24P11.120
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49856
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49856
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <SCH>
A;Cross-references: EMBL:AL356833; GSPDB:GN00116; NCSP:B24P11.120
A;Experimental source: BAC clone B24P11; strain OR74A
C;Genetics:
A;Gene: NCSP:B24P11.120
A;Map position: 6
A;Introns: 79/3

Query Match 56.5%; Score 35; DB 2; Length 240;
Best Local Similarity 54.5%; Pred. No. 81;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPQQLTKQ 11
|||:|:|:
Db 156 CRVQDDTRG 166

RESULT 28
C70873
probable enoyl-CoA hydratase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: C70873
R;Cole, S.I.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70873
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-285 <COL>
A;Cross-references: GB:AL021184; GB:AL123456; NID:G3261498; PIDN:CRA16000.1; PID:g279140
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: echA12
C;Superfamily: naphthoate synthase; enoyl-CoA hydratase homology
F:41-201/Domain: enoyl-CoA hydratase homology <ECH>

Query Match 56.5%; Score 35; DB 1; Length 285;

Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQLTKQ 10
|||:|:|:
Db 226 RPIELTKR 234

RESULT 29
AH2016
Hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 24-Nov-2003
C;Accession: AH2016
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yanada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2016
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <KUE>
A;Cross-references: GB:BA000019; PIDN:BA78052.1; PID:gl7135506; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1686
C;Superfamily: tartrate-resistant acid phosphatase

Query Match 56.5%; Score 35; DB 2; Length 303;
Best Local Similarity 70.0%; Pred. No. 99;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQQLTKQ 11
|||:|:|:
Db 104 RPYQLTKQ 113

RESULT 30
T14058
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Neolamprologus brichardi
C;Species: Neolamprologus brichardi
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: T14058
R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
Mol. Phylogenet. Evol. 4, 420-432, 1995
A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
A;Reference number: Z17790; MUID:96360498; PMID:8747298
A;Accession: T14058
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-348 <KOC>
A;Cross-references: EMBL:U07255; NID:g463956; PID:g463957; PIDN:AAC59804.1
A;Experimental source: strain T47a; isolate PSU
C;Genetics:
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQ 11
|||:|:|:
Db 267 QELTKQ 273

RESULT 31
T14034
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Julidochromis marlieri
C;Species: mitochondrion Julidochromis marlieri

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C;Accession: T14034
 R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A;Reference number: Z17790; MUID:96360498; PMID:8747298
 A;Accession: T14034
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-348 <KOC>
 A;Cross-references: EMBL:U07249; NID:G463944; PID:G463945; PIDN:AAC59798.1
 A;Experimental source: strain T1a; PSU
 C;Genetics:
 A;Genome: mitochondrion
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
 Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QELTKQG 11
 Db 267 QELTKQG 273

RESULT 32
 T14206
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Tanganicodus irsacae mitochondrion
 C;Species: mitochondrion Tanganicodus irsacae
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C;Accession: T14206
 R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A;Reference number: Z17790; MUID:96360498; PMID:8747298
 A;Accession: T14206
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-348 <KOC>
 A;Cross-references: EMBL:U07265; NID:G463976; PID:G463977; PIDN:AAC59814.1
 A;Experimental source: strain T13a; PSU
 C;Genetics:
 A;Genome: mitochondrion
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
 Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QELTKQG 11
 Db 267 QELTKQG 273

RESULT 33
 T14118
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Nile tilapia mitochondrion
 C;Species: mitochondrion Tilapia nilotica, Oreochromis niloticus (Nile tilapia)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C;Accession: T14118
 R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A;Reference number: Z17790; MUID:96360498; PMID:8747298
 A;Accession: T14118
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-348 <KOC>
 A;Cross-references: EMBL:U07258; NID:G463962; PID:G463963; PIDN:AAC59806.1
 A;Experimental source: strain T77a; isolate PSU
 C;Genetics:

A;Genome: mitochondrion
 A;Genetic code: SGC1
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
 Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QELTKQG 11
 Db 267 QELTKQG 273

RESULT 34
 T14140
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Perissodus microlepis mitochondrion
 C;Species: mitochondrion Perissodus microlepis
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C;Accession: T14140
 R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A;Reference number: Z17790; MUID:96360498; PMID:8747298
 A;Accession: T14140
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-348 <KOC>
 A;Cross-references: EMBL:U07260; NID:G463966; PID:G463967; PIDN:AAC59809.1
 A;Experimental source: strain T32a; PSU
 C;Genetics:
 A;Genome: mitochondrion
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
 Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QELTKQG 11
 Db 267 QELTKQG 273

RESULT 35
 T14128
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Paracyprichromis brieni mitochondrion
 C;Species: mitochondrion Paracyprichromis brieni
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C;Accession: T14128
 R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A;Reference number: Z17790; MUID:96360498; PMID:8747298
 A;Accession: T14128
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-348 <KOC>
 A;Cross-references: EMBL:U07259; NID:G463964; PID:G463965; PIDN:AAC59808.1
 A;Experimental source: strain T40a; isolate PSU
 C;Genetics:
 A;Genome: mitochondrion
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
 Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QELTKQG 11
 Db 267 QELTKQG 273

RESULT 36

T13839
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Buccochromis lepturus mitochondrion
 C:Species: mitochondrion Buccochromis lepturus
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C:Accession: T13839
 R:Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A:Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A:Reference number: Z17790; MUID:96360498; PMID:8747298
 A:Accession: T13839
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-348 <KOC>
 A:Cross-references: EMBL:U07241; NID:G463928; PID:G463929; PIDN:AAC59788.1
 A:Experimental source: strain JAC 2
 C:Genetics:

A:Genome: mitochondrion
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11
 |||||
 Db 267 QELTKQG 273

RESULT 37

T14122
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Ophthalmotilapia ventralis mitochondrion
 C:Species: mitochondrion Ophthalmotilapia ventralis
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C:Accession: T14122
 R:Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A:Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A:Reference number: Z17790; MUID:96360498; PMID:8747298
 A:Accession: T14122
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-348 <KOC>
 A:Cross-references: EMBL:U07257; NID:G463960; PID:G463961; PIDN:AAC59807.1
 A:Experimental source: strain T10a; isolate PSU
 C:Genetics:

A:Genome: mitochondrion
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11
 |||||
 Db 267 QELTKQG 273

RESULT 38

T14209
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Telmatochromis temporalis mitochondrion
 C:Species: mitochondrion Telmatochromis temporalis
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C:Accession: T14209
 R:Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A:Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A:Reference number: Z17790; MUID:96360498; PMID:8747298
 A:Accession: T14209

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-348 <KOC>
 A:Cross-references: EMBL:U07266; NID:G463978; PID:G463979; PIDN:AAC59817.1
 A:Experimental source: strain T49a; PSU
 C:Genetics:

A:Genome: mitochondrion
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11
 |||||
 Db 267 QELTKQG 273

RESULT 39

T14216
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Xenotilapia flavipinnus mitochondrion
 C:Species: mitochondrion Xenotilapia flavipinnus
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C:Accession: T14216
 R:Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A:Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A:Reference number: Z17790; MUID:96360498; PMID:8747298
 A:Accession: T14216
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-348 <KOC>
 A:Cross-references: EMBL:U07269; NID:G463984; PID:G463985; PIDN:AAC59818.1
 A:Experimental source: strain T12a; PSU
 C:Genetics:

A:Genome: mitochondrion
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11
 |||||
 Db 267 QELTKQG 273

RESULT 40

T14200
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Pseudotropheus sp. mitochondrion
 C:Species: mitochondrion Pseudotropheus sp.
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C:Accession: T14200
 R:Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
 Mol. Phylogenet. Evol. 4, 420-432, 1995
 A:Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
 A:Reference number: Z17790; MUID:96360498; PMID:8747298
 A:Accession: T14200

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-348 <KOC>
 A:Cross-references: EMBL:U07263; NID:G463972; PID:G463973; PIDN:AAC59812.1

A:Genome: mitochondrion
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu May 6 08:16:50 2004

us-10-067-122b-2_copy_105_115.rpr

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Qy 5 QELTKOG 11
Db |||||
267 QELTKOG 273

Search completed: May 5, 2004, 14:41:21
Job time : 1.31849 secs

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:56 ; Search time 0.866438 Seconds
(without alignments)
661.065 Million cell updates/sec

Title: US-10-067-122B-2_COPY_105_115
Perfect score: 62
Sequence: 1 CRPGELTQKG 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	256	1 TNR9 MOUSE	P20334 mus musculus
2	47	75.8	255	1 TNR9 HUMAN	Q07011 homo sapien
3	42	67.7	639	1 BMP3 STRPU	P98059 strongyloce
4	40	64.5	297	1 XEDA HUMAN	Q9hav5 homo sapien
5	39	62.9	228	1 TR18 MOUSE	Q35714 mus musculus
6	39	62.9	684	1 NTF2 MCV1	Q98218 molluscum c
7	38	61.3	413	1 NCAP IHNV	P46951 infectious
8	38	61.3	672	1 PKX5 MOUSE	P08399 mus musculus
9	37	59.7	416	1 TR19 MOUSE	Q9j113 mus musculus
10	37	59.7	423	1 TR19 HUMAN	Q9ns68 homo sapien
11	37	59.7	514	1 EDAR ORYLA	Q90v72 oryzias lat
12	37	59.7	515	1 YMB0 YEAST	Q03264 saccharomyc
13	37	59.7	876	1 KCH8 MOUSE	P59111 mus musculus
14	37	59.7	986	1 Z445 MOUSE	Q8z213 mus musculus
15	37	59.7	1031	1 Z445 HUMAN	P59923 mus sapien
16	37	59.7	1102	1 KCH8 RAT	Q9qws8 rattus norv
17	37	59.7	1107	1 KCH8 HUMAN	Q96142 homo sapien
18	37	59.7	2871	1 FBN1 MOUSE	Q61554 mus musculus
19	36.5	58.9	372	1 R54 ANASP	Q9m841 arabidopsis
20	36	58.1	202	1 NCAP VHSVO	Q8yt10 anabaena sp
21	36	58.1	404	1 NCAP VHSVM	P24378 viral hemor
22	36	58.1	404	1 EBB2 CHICK	P27371 viral hemor
23	36	58.1	1004	1 EBB2 CHICK	P28693 gallus gall
24	36	58.1	1075	1 MTR3 MOUSE	Q8k296 mus musculus
25	36	58.1	1198	1 MTR3 HUMAN	Q13615 homo sapien
26	35	56.5	129	1 ATPZ VIBAL	P12983 vibrio algi
27	35	56.5	285	1 ECHC MYCTU	O53163 mycobacteri
28	35	56.5	349	1 N2UM ONCMY	P48175 oncorhynch
29	35	56.5	349	1 N2UM SALSA	Q35924 salmo salar
30	35	56.5	385	1 ARGD THEM	Q3x2a5 thermotoga
31	35	56.5	705	1 C1R HUMAN	P00736 homo sapien
32	35	56.5	887	1 MCM2 DROME	P49735 drosophila
33	35	56.5	1342	1 RPOB_BUCAP	P41184 buchnera ap

34 35 56.5 1744 1 TENS_CHICK Q04205 gallus gall
35 34 54.8 134 1 LEG4_CHICK P07583 gallus gall
36 34 54.8 218 1 IM23_SCHJA P27591 schistosoma
37 34 54.8 219 1 END3_BAGSU P39788 bacillus su
38 34 54.8 225 1 AFQ1_STRCO Q04942 streptomyce
39 34 54.8 241 1 TEL8_HUMAN O9y5u5 homo sapien
40 34 54.8 315 1 MAC9_HUMAN P43382 homo sapien
41 34 54.8 374 1 TGT_YERPE Q8zc33 yersinia pe
42 34 54.8 375 1 TGT_ECOLI P19675 escherichia
43 34 54.8 375 1 TGT_SALTI Q8z8y0 salmonella
44 34 54.8 375 1 TGT_SALTY Q8zr48 salmonella
45 34 54.8 375 1 TGT_SHIFL Q54177 shigella fl

ALIGNMENTS

RESULT 1
TNR9 MOUSE
ID TNR9 MOUSE STANDARD; PRT; 256 AA.
AC P20334;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184547; PubMed=2784565;
RA Kwon B.S., Weissman S.M.;
RT "cDNA sequences of two inducible T-cell. Genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=94179805; PubMed=8133039;
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
RT antigen 4-1BB.";
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 25-29.
RX MEDLINE=93139510; PubMed=7678621;
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
RA Kwon B.S.;
RT "Inducible T cell antigen 4-1BB. Analysis of expression and
RT function.";
RL J. Immunol. 150:771-781(1993).
CC -!- FUNCTION: Receptor for TNFRSF14/4-1BBL. Possibly active during T
CC cell activation.
CC -!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC ASSOCIATES WITH P56-LCK. Interacts with TRAF1, TRAF2 AND TRAF3 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC -!- INDUCTION: Optimal by PMA and ionomycin.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
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CC -----
CC EMBL; J04492; AAA40167.1; -;
CC EMBL; U02567; AAA93113.1; -;
CC -----
CC DR

DR PIR; B32393; B32393.
 DR PIR; 1D07; 26-SEP-01.
 DR MGI; 1101059; Tnfrsf9.
 DR InterPro; IPR001368; TNFR C6.
 DR Pfam; PF00020; TNFR C6; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00652; TNFR_NGFR_2; FALSE NEG.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 256
 FT DOMAIN 25 187
 FT TRANSMEM 188 208
 FT DOMAIN 209 256
 FT REPEAT 17 45
 FT REPEAT 46 85
 FT REPEAT 86 117
 FT REPEAT 118 159
 FT DISULFID 28 37
 FT DISULFID 31 44
 FT DISULFID 47 61
 FT DISULFID 64 77
 FT DISULFID 67 85
 FT DISULFID 87 93
 FT DISULFID 98 105
 FT DISULFID 101 116
 FT DISULFID 119 133
 FT DISULFID 139 158
 FT CARBOHYD 128 138
 FT CARBOHYD 138 138
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03G60813C4 CRC64;
 Query Match 100.0%; Score 62; DB 1; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPGQELTKQG 11
 DB 105 CRPGQELTKQG 115
 RESULT 2
 TNFR9_HUMAN STANDARD; PRT; 255 AA.
 AC Q07011;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen IIA) (CD137 antigen).
 DE (CD137 antigen).
 GN TNFRSF9 OR IIA OR CD137.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=94374434; PubMed=8088337;
 RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Rous E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
 RA "Molecular and biological characterization of human 4-1BB and its ligand."
 RT Eur. J. Immunol. 24:2219-2227(1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=94085794; PubMed=8262389;
 RA Schwarz H., Tuckwell J., Lotz M.;
 RA "A receptor..."

RT family."
 RL Gene 134:295-298(1993).
 RN [3]
 RP REVISION TO 107.
 RA Schwarz H.;
 RP Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95347766; PubMed=7622190;
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
 RA "Characterization of human homologue of 4-1BB and its ligand."
 RL Immunol. Lett. 45:67-73(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC Pearce A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
 RX MEDLINE=98078711; PubMed=9418902;
 RA Arch R.H., Thompson C.B.;
 RT "4-1BB and Oxa4 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB."
 RL Mol. Cell. Biol. 18:558-565(1998).
 RN [8]
 RP INTERACTION WITH TRAF1 AND TRAF2.
 RX MEDLINE=98270914; PubMed=9607925;
 RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
 RA Goldstein M.D., Bangia N., Dehenadette M.A., Mak T.W., Choi Y.,
 RA Watts T.H.;
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by 4-1BB ligand."
 RL J. Exp. Med. 187:1849-1862(1998).
 RN [9]
 RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
 RX MEDLINE=21662677; PubMed=11804328;
 RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
 RA "A novel leucine-rich repeat protein (LRR-1): potential involvement in 4-1BB-mediated signal transduction."
 RL Mol. Cells 12:304-312(2001).
 CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with TRAF-repeat protein 1/LRR-1.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDW137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
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CC -----
CC EMBL; U03397; AAA33133.1; -.
CC EMBL; L12964; AAA62478.2; -.
CC EMBL; AL009183; CAB57398.1; -.
CC EMBL; BC006196; AAH06196.1; -.
CC PIR; I38426; I38426.
CC Genew; HGNC:11324; TNFRSF9.
CC MIM; 602250; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:004872; F:receptor activity; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:000285; P:negative regulation of cell proliferation; TAS.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS0050; TNFR_NGFR_2; 1.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 18 186 SUPRAFAMILY MEMBER 9.
FT TRANSMEM 187 213 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 214 255 POTENTIAL.
FT REPEAT 17 45 CYTOPLASMIC (POTENTIAL).
FT REPEAT 47 86 TNFR-CYS 1.
FT REPEAT 87 118 TNFR-CYS 2.
FT REPEAT 119 159 TNFR-CYS 3.
FT REPEAT 120 199 TNFR-CYS 4.
FT DOMAIN 214 255 INTERACTS WITH LRR-1.
FT DISULFID 28 37 BY SIMILARITY.
FT DISULFID 31 45 BY SIMILARITY.
FT DISULFID 48 62 BY SIMILARITY.
FT DISULFID 65 78 BY SIMILARITY.
FT DISULFID 88 96 BY SIMILARITY.
FT DISULFID 99 106 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 121 133 BY SIMILARITY.
FT DISULFID 139 158 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;

Query Match 75.8%; Score 47; DB 1; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGQELTKQG 11
Db 106 CRGQELTKKG 116

RESULT 3
BMPH STRPU STANDARD; PRT; 639 AA.
AC F98069;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 1 homolog precursor (EC 3.4.24.-) (SUBMP).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinolidea; Euechinolidea; Echinoidea; Echinoida; Strongylocentrotidae;

OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=94215496; PubMed=8162855;
RX Hwang S.P.L., Partin J.S., Lennarz W.J.;
RT "Characterization of a homolog of human bone morphogenetic protein 1
in the embryo of the sea urchin, Strongylocentrotus purpuratus.";
RL Development 120:559-568(1994).
CC -!- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in
hatched blastula.
CC -!- DEVELOPMENTAL STAGE: Embryo; highest level before spiculogenesis.
CC -!- SIMILARITY: Belongs to peptidase family M12A.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -----
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CC -----
CC EMBL; L23838; AAA30081.1; -.
CC HSSP; P00736; LAPQ.
CC MEROPS; M12.005; -.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000859; CUB_Ca.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR006026; Peptidase_M.
CC Pfam; PF01400; Astacin; 1.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00008; EGF; 1.
CC PRINTS; P00480; ASTACIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00179; EGF_Ca; 1.
CC SMART; SM00235; ZnMG; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS01187; EGF_Ca; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;
KW Metalloprotease; EGF-like domain; Calcium; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 109 POTENTIAL.
FT CHAIN 110 639 BONE MORPHOGENETIC PROTEIN 1 HOMOLOG.
FT DOMAIN 110 306 METALLOPROTEASE.
FT DOMAIN 307 419 CUB 1.
FT DOMAIN 420 531 CUB 2.
FT DOMAIN 532 573 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT METAL 197 197 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 198 198 BY SIMILARITY.
FT METAL 201 201 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 207 207 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 536 548 BY SIMILARITY.
FT DISULFID 544 557 BY SIMILARITY.
FT DISULFID 559 572 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 317 317 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 639 AA; 71893 MW; 59307B265B7894AD CRC64;

Query Match 67.7%; Score 42; DB 1; Length 639;
Best Local Similarity 63.6%; Pred. No. 3.9;

GO: GO:0008544; P:epidermal differentiation; NAS.

InterPro; IPR001368; TNFR_c6.
Pfam; PF00200; TNFR_c6; 2.
SMART; SMC0208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_2; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Developmental protein; Differentiation; Transmembrane;
Glycoprotein; Repeat.
DOMAIN 1 138
FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
TRANSMEM 139 159
(POTENTIAL).
DOMAIN 160 297
REPEAT 2 41
REPEAT 43 83
REPEAT 85 118
REPEAT 85 118
DISULFID 3 15
DISULFID 18 31
DISULFID 21 41
DISULFID 44 58
DISULFID 61 75
DISULFID 64 83
DISULFID 86 104
DISULFID 107 118
CARBOHYD 74 74
MUTAGEN 256 256
SEQUENCE 297 AA; 32728 MW; OE71127C6C48240C CRC64;
Score 40; DB 1; Length 297;
Best Local Similarity 77.8%; Pred. No. 4.1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 1

QY 1 CRPGQELTK 9
DDB 21 CGFGQELSK 29

RESULT 5
TR18_MOUSE STANDARD; PRT; 228 AA.
IID TR18_MOUSE STANDARD; PRT; 228 AA.
O35714; O9JKR1; O9JKR2; O9JKR3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 18 precursor
(Glucocorticoid-induced TNFR-related protein).
TNFRSF18 OR GITR.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
(1)
SEQUENCE FROM N.A. (ISOFORM A).
STRAIN=C3H;
MEDLINE=973232352; PubMed=9177197;
Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
Moraza R., Migliorati G., Riccardi C.;
"A new member of the tumor necrosis factor/nerve growth factor
receptor family inhibits T cell receptor-induced apoptosis";
Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
(2)
SEQUENCE FROM N.A. (ISOFORM A).
STRAIN=BALB/c;
MEDLINE=20256302; PubMed=10798444;
Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Delfino D., Migliorati G., Riccardi C.;
"Gene structure and chromosomal assignment of mouse GITR, a member of
the tumor necrosis factor/nerve growth factor receptor family";
DNA Cell Biol. 19:205-217(2000).
(3)
SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
STRAIN=Thymus;
MEDLINE=20292073; PubMed=10836847;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,


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FT NP_BIND 197 204 ATP (BY SIMILARITY).
FT SITE 308 311 DEXH BOX.
SQ SEQUENCE 684 AA; 76556 MW; 51072B193CCC7284 CRC64;

Query Match 62.9%; Score 39; DB 1; Length 684;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQLTKQ 11
Db 117 CRPGLEAREG 127

RESULT 7
NCAP_IHNV
ID NCAP_IHNV STANDARD; PRT; 413 AA.
AC P19691;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Infectious hematopoietic necrosis virus (strain Round Butte) (IHNV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11291;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8907371; PubMed=3201758;
RA Gilmore R.D. Jr., Leong J.C.;
RT "The nucleocapsid gene of infectious hematopoietic necrosis virus, a fish rhabdovirus."
RL Virology 167:644-648(1988).
CC -!- PUM: Phosphorylated.
CC -!- SIMILARITY: TO VHSV NUCLEOCAPSID PROTEIN.
CC
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CC
CC EMBL; J04321; AAA46240.1; -.
DR PIR; A31834; VHVNIH.
DR InterPro; IPR004902; Rhabdo.ncap.2.
DR Pfam; PF03216; Rhabdo.ncap.2.1.
KW Nucleocapsid; Phosphorylation.
SQ SEQUENCE 413 AA; 45700 MW; 5E2AFF659BBEE38 CRC64;

Query Match 61.3%; Score 38; DB 1; Length 413;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQGLTK 9
Db 183 RPQGLTK 190

RESULT 8
PHX5 MOUSE
ID PHX5 MOUSE STANDARD; PRT; 672 AA.
AC P08399;
DT 01-AUG-1998 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Per-hexamer repeat protein 5.
GN PHX5 OR PER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN SEQUENCE FROM N.A.
RP MEDLINE=86014384; PubMed=2413365;
RX Shin H.S., Bargiello T.A., Clark B.T., Jackson F.R., Young M.W.;
RA "An unusual coding sequence from a Drosophila clock gene is conserved
RT in vertebrates."
RL Nature 317:445-448(1985).
CC -!- SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M12039; AAA88320.1; -.
DR EMBL; X02966; CAA26710.2; -.
DR PIR; A24403; UMMS.
DR MGD; MGI:104521; Phx5.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
KW Repeat.
FT DOMAIN 59 672 G-T REPEATS.
SQ SEQUENCE 672 AA; 57924 MW; E85BF428CF424C0B CRC64;

Query Match 61.3%; Score 38; DB 1; Length 672;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQLTK 9
Db 23 CRPGLEAK 31

RESULT 9
TR19 MOUSE
ID TR19 MOUSE STANDARD; PRT; 416 AA.
AC Q9JLL3; Q9JHF1; Q9JUH6; Q9JUL2; Q9QXW7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 19 precursor
DE (Toxicity and JNK inducer) (TRADE).
GN TNFRSF19 OR TR19 OR TAJ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RX MEDLINE=20054362; PubMed=10585776;
RA Hu S., Tanada K., Ni J., Vincenz C., Chen L.;
RT "Characterization of TNFRSF19, a novel member of tumor necrosis factor
RT receptor superfamily."
RL Genomics 62:103-107(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Embryo, and Spleen;
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a novel member of the tumor necrosis factor receptor family,
RT activates the c-Jun N-terminal kinase pathway and mediates
RT caspase-independent cell death."
RL J. Biol. Chem. 275:15336-15342(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RC TISSUE=Brain;
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.;

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RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6;
RA Chaudhary D., Long A.J.;
RT "TRADE, a novel TNF receptor family member associated with death
RT signaling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Can mediate activation of c-Jun and NF-kappa-B. May
CC promote caspase-independent cell death (By similarity). Isoform 2
CC and isoform 3 may act as decoy receptors.
CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3 and TRAF5 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 3 and
CC 4); secreted (isoform 2) (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=TAJ-alphaL; Sequence=Displayed;
CC IsoId=Q9JLL3-1; Sequence=VSP_006515;
CC Name=2; Synonyms=TAJ-betaL;
CC IsoId=Q9JLL3-2; Sequence=VSP_006513;
CC Name=3; Synonyms=TAJ-alphaS, dTROY;
CC IsoId=Q9JLL3-3; Sequence=VSP_006516;
CC Name=4;
CC IsoId=Q9JLL3-4; Sequence=VSP_006517;
CC -1- TISSUE SPECIFICITY: Highly expressed in adult brain, and in
CC embryos from day 11-17, but not earlier. Detected in embryonic
CC brain and epithelium, and at lower levels in adult heart, lung and
CC liver. In neonatal mice, mainly in hair follicles and neuron-like
CC cells in the cerebellum, but not in the skin epidermis. Isoform 3
CC was found in embryonic day 17.5 skin but not in brain and liver.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC
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CC
CC EMBL; AF173166; AAF19795.1; -
CC EMBL; AF167552; AAF71825.1; -
CC EMBL; AF167554; AAF71827.1; -
CC EMBL; AF167553; AAF71826.1; -
CC EMBL; AB040432; BAB03267.1; -
CC EMBL; AB040433; BAB03268.1; -
CC EMBL; AF247000; AAK28397.1; -
CC MGB; MGI:1352474; Tnfrsf19.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC SMART; SMO0208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 416
FT
FT POTENTIAL.
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPRACELLULAR MEMBER 19.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 191
FT DOMAIN 192 416
FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 33 72
FT TNFR-CYS 1.
FT REPEAT 74 114
FT TNFR-CYS 2.
FT REPEAT 116 149
FT TNFR-CYS 3 (PARTIAL).
FT DISULFID 34 46
FT BY SIMILARITY.
FT DISULFID 49 62
FT BY SIMILARITY.
FT DISULFID 52 72
FT BY SIMILARITY.
FT DISULFID 75 89
FT BY SIMILARITY.

FT DISULFID 92 106
FT BY SIMILARITY.
FT DISULFID 95 114
FT BY SIMILARITY.
FT DISULFID 117 135
FT BY SIMILARITY.
FT DISULFID 138 149
FT N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 105 105
FT T -> E (in isoform 2).
FT VARSPLIC 150 150
FT /FTid=VSP_006513.
FT Missing (in isoform 2).
FT /FTid=VSP_006514.
FT WSLRSQDIQYN -> CKLPSLCLTVK (in isoform
FT 3).
FT /FTid=VSP_006515.
FT Missing (in isoform 3).
FT /FTid=VSP_006516.
FT NESTASLDS -> MLCFRFDL (in isoform 4).
FT VARSPLIC 340 348
FT /FTid=VSP_006517.
FT Missing (in isoform 4).
FT VARSPLIC 349 416
FT /FTid=VSP_006518.
FT CONFLICT 31 31
FT T -> A (IN REF. 1).
FT CONFLICT 208 208
FT S -> P (IN REF. 1).
FT CONFLICT 287 287
FT N -> D (IN REF. 3).
FT CONFLICT 343 343
FT T -> A (IN REF. 3).
SQ SEQUENCE 416 AA; 45294 MW; 19CA2F75DD7B9D49 CRC64;
Query Match 59.7%; Score 37; DB 1; Length 416;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CRPGQELTKQ 10
DB 52 CGPGWELSK 61
RESULT 10
TR19 HUMAN
ID TR19 HUMAN STANDARD; PRT; 423 AA.
AC Q9NS58; Q9BXZ9; Q9BY00; Q9NZV2;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 19 precursor
DE (Toxicity and JNK inducer) (TRADE).
GN TNFRSF19 OR TROY OR TAJ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2;
RP TRAF3 AND TRAF5.
RC TISSUE=Petal spleen;
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a novel member of the tumor necrosis factor receptor family,
RT activates the c-Jun N-terminal kinase pathway and mediates
RT caspase-independent cell death.";
RL J. Biol. Chem. 275:15336-15342(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Glial tumor;
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Chaudhary D., Long A.J.;
RT "TRADE, a novel TNF receptor family member associated with death
RT signaling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

